

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 7, 2004, 04:47:28 ; Search time 4615 Seconds

(without alignments)  
2090.379 Million cell updates/sec

Title: US-10-071-174-2

Perfect score: 1084

Sequence: 1 MYDQRLRTMADPLRERTE.....QAFLSCLLTAFIYLWTELL 204

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastp -SUFFIX=rg -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb\_htg.\*

3: gb\_in.\*

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5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_scs.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1084	100.0	615	9 AF285092	AF285092 Homo sapi
2	1084	100.0	887	9 AF326964	AF326964 Homo sapi
3	1045	96.4	1168	6 BD233466	BD233466 Human pro
4	1036.5	95.6	726	6 CQ752105	CQ752105 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	1035	95.5	582	6	BD233456	Human pro	
6	1035	95.5	585	9	HS458330	Homo sapi	
C	7	855	78.9	9	AC023906	Homo sapi	
8	494	45.6	214669	2	AC018903	Homo sapi	
9	487	44.9	1074	10	AY029163	Rattus no	
10	474.5	43.8	1209	10	AF102501	Mus muscu	
11	474.5	43.8	1225	10	AF067660	Mus muscu	
12	467.5	43.1	1257	10	BC052690	Mus muscu	
13	342	31.5	240461	2	AC111669	Rattus no	
14	333.5	30.8	169914	2	AC133947	Mus muscu	
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17	193.5	17.9	1475	5	CCNR13	C. coturnix	
18	188.5	17.4	534	5	AF375661	Gallus ga	
19	179	16.5	531	5	AF441285	Danio rer	
C	20	178.5	16.5	151102	14	AF282130	Meleagrid
21	178.5	16.5	159160	14	AF291866	Meleagrid	
C	22	178.5	16.5	159160	14	AF291866	Meleagrid
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24	143.5	13.2	636	5	AF120210	Gallus ga	
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27	132	12.2	243686	2	AC096430	Rattus no	
28	131	12.1	694	4	AB080230	Canis fam	
29	129	11.9	658	6	AX525910	Sequence	
30	127	11.7	558	9	HS4417988	Homo sapi	
31	127	11.7	579	6	E58778	Screening m	
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40	127	11.7	996	6	AR429416	Sequence	
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43	125	11.5	525	5	AF120211	Gallus ga	
44	125	11.5	624	6	AR027309	Sequence	
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ALIGNMENTS

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DEFINITION	AF285092	Homo sapiens Bcl-2-like protein	10	mrna	complete cds.	
ACCESSION	AF285092	Homo sapiens Bcl-2-like protein	10	mrna	complete cds.	
VERSION	AF285092.1	GI:9837265				
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS		Zhang, H., Holzgrev, W. and De Geyter, C.				
TITLE		Bcl-2-L-10, a novel anti-apoptotic member of the Bcl-2 family, blocks apoptosis in the mitochondria death pathway but not in the death receptor pathway				
JOURNAL		Hum. Mol. Genet. 10 (21), 2329-2339 (2001)				
MEDLINE		21548034				
PUBMED		11689480				
REFERENCE		2 (bases 1 to 615)				
AUTHORS		Zhang, H.H.				
TITLE		Direct Submission				
JOURNAL		Submitted (05-JUL-2000) University Women's Hospital, Schanzenstra				
FEATURES		46, Basel 4057, Switzerland				
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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QY 21 LeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40
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QY 41 ProSerThrProGluAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHis 60
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QY 61 ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu 80
DB 181 CGGTCTCTTTTCTCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGG 240
QY 81 MetAlaAspSerValLeuSerAspSerProGlyProThrTyrGlyArgValValThrLeu 100
DB 241 ATGGCGGATTCCTGCTCTCCGACAGCGCGCGCGCGCGCGCGCGAGTGGTGAGCTC 300
QY 101 ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTrpLysLys 120
DB 301 GTACCTTCGCGAGGAGCGCTGCTGGAGAGGCGCGCTGCTGACCCCGCGTGGAGAG 360
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RESULT 2

AF326964

LOCUS

DEFINITION Homo sapiens BCL2 (BCL2) mRNA, complete cds. PRI 01-MAY-2001

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AF326964
AF326964.1 GI:13898393
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
Ke,N., Godzik,A. and Reed,J.C.
Bcl-2, a novel Bcl-2 family member that differentially binds and
regulates Bax and Bak
J. Biol. Chem. 276 (16), 12481-12484 (2001)
21201065
MEDLINE
11278245
REFERENCE
2 (bases 1 to 887)
Ke,N., Godzik,A. and Reed,J.C.
Direct Submission
TITLE
Submitted (07-DEC-2000) The Burnham Institute, 10901 N. Torrey
Pines Rd., La Jolla, CA 92037, USA
JOURNAL
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ORIGIN
Alignment Scores:
Pred. No.: 6,57e-81 Length: 887
Score: 1084.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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QY 1 MetValAspGlnLeuArgGluArgThrThrMetAlaAspProLeuArgGluArgThrGlu 20
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QY 21 LeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40
DB 110 CTGTTGCTGGCGGACTACCTGGGGTACTGGCCCGGGAACCGGACCCCGGAGCGCGC 169
QY 41 ProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHis 60
DB 170 CCATCCAGCGCGGAGCGCGCTGCTGGCTCGCGCGCGCGCGAGTTACGGAGTTAC 229
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DB 290 ATGGCGGATTCCTGCTCTCCGACAGCGCGCGCGCGCGCGAGTGGTGGAGCTC 349
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Db 410 TGGGGCTTCACGCGCGGCTAAAGGAGCAGGAGGCGGACGCTGCCCGGAGCTGCCAGGCG 469
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Db 470 CTGGTGGCTTCCTGAGCTCGCGGCTCAATGGGGCAGCACCGCGCTGGCTGCGAGCTCAG 529
Qy 161 GlyGlyTrpAspGlyPheCysHisPhePheArgTrpProPheProLeuAlaPheTrpArg 180
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Qy 181 LysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrThrAlaPheLeuTrpLeuTrp 200
Db 590 AAACAGCTGGTCCAGGCTTTTGTCTCATGCTGTGTTAAACAACAGCTTCATTATCTCTGG 649
Qy 201 ThrArgLeuLeu 204
Db 650 ACACGATTATTA 661

RESULT 3
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LOCUS Human protein having hydrophobic domain and DNA encoding the same.
DEFINITION Human protein having hydrophobic domain and DNA encoding the same.
ACCESSION BD233466
VERSION BD233466.1 GI:33043236
KEYWORDS JP 2002519016-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLES Kato, S. and Kimura, T.
JOURNAL Human protein having hydrophobic domain and DNA encoding the same
COMMENT Patient: JP 2002519016-A 12 02-JUL-2002;
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS Homo sapiens (human)
PN JP 2002519016-A/12
PD 02-JUL-2002 JP 2000557267
PF 18-JUN-1999 JP 2000557267
PI SEISHI KATO, TOMOKO KIMURA
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N5/00, C12N5/ PC
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FT source 1. 1168
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Source 1. 1168
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Query Match: 96.40% Indels: 0
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US-10-071-174-2 (1-204) x BD233466 (1-1168)

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Db 361 GAGCAGAGGGCGGACGTCGCCCGGACTGCCAGCGCTGGTGCGCTTGTGAGCTCGCGG 420
Qy 149 LeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrpAspGlyPheCysHis 168
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Qy 169 PhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeu 188
Db 481 TTCCTCAGGACCCCTTCCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTG 540
Qy 189 SerCysLeuLeuThrThrAlaPheLeuTrpLeuTrpThrArgLeuLeu 204
Db 541 TCATGCTTGTAAACACAGCGCTTCATTATCTCTGGACAGATTATTA 588

RESULT 4
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LOCUS Sequence 38039 from Patent WO02068579.
DEFINITION CQ752105
ACCESSION CQ752105
VERSION CQ752105.1 GI:42387450
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLES Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
JOURNAL Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 38039 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
Source 1. 726
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Pred. No.: 4.66e-77 Length: 726
Score: 1036.50 Matches: 203
Percent Similarity: 89.04% Conservatives: 0
Best Local Similarity: 89.04% Mismatches: 1
Query Match: 95.62% Indels: 24
DB: 6 Gaps: 1
US-10-071-174-2 (1-204) x CQ752105 (1-726)

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QY 197 eTyrLeuTrpThrArgLeuLeu 204
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RESULT 5
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LOCUS Human protein having hydrophobic domain and DNA encoding the same.
DEFINITION BD233456
ACCESSION BD233456.1 GI:33043226
VERSION JP 2002519016-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Kato, S. and Kimura, T.
Human protein having hydrophobic domain and DNA encoding the same
Patent: JP 2002519016-A 2 02-JUL-2002;
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS Homo sapiens (human)
PN JP 2002519016-A/2
PD 02-JUL-2002
PF 18-JUN-1999 JP 2000557267
PI SEISHI KATO, TOMOKO KIMURA
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N5/00, C12N5/ PC
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CC same
PH Key Location/Qualifiers
FT source 1.582

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QY 51 SerAlaAlaAlaArgLeuArgGlnIleHisArgSerPhePheSerAlaTyrLeuGlyTyr 70
Db 121 TCCGCGCGCGCGAGGTACGGCAGATTACCGTCTCTTTTCTCCGCTACCTCGGCTAC 180
QY 71 ProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerPro 90
Db 181 CCGCGGAACCGCTTCGAGCTGGTGGCGCTGATGCCGAGATTCCTGTCTCCGACAGCC 240
QY 91 GlyProThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArg 110
Db 241 GCGCCACCTCGGCGCAGAGTGGTACGCTCGTACCTTCGACGAGCGCTGGTGGAGAGA 300
QY 111 GlyProLeuValThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGln 130
Db 301 GGGCGCTGGTGGCGCGCGCTGGAGAGTGGGGCTTCAGCGCGCGGCTAAAGAGCAG 360
QY 131 GluGlyAspValAlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArgLeuMet 150
Db 361 GAGGCGACGCTCGCGCGGACTGCCAGCGCTGGTGGCGCTTCGAGCTCGCGGCTCATG 420
QY 151 GlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyLysTrpAspGlyPheCysHisPhePhe 170
Db 421 GGGCAGCAGCGCGCTGGCTGCGAGCTCAGGCGCGCTGGGATGGCTTTTGTCACTTCTC 480
QY 171 ArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCys 190
Db 481 AGGACCCCTTTCACCTGGCTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTATGC 540
QY 191 LeuLeuThrThrAlaPheIleTyrLeuTrpThrArgLeuLeu 204
Db 541 TTGTTAACACAGCCTTCATTATCTCTGGACACGATTATTA 582

RESULT 6
HSA458330 585 bp DNA linear PRI 25-APR-2002
LOCUS Homo sapiens NRH gene for anti-apoptotic protein.
DEFINITION HSA458330
ACCESSION AJ458330
VERSION AJ458330.1 GI:20338765
KEYWORDS anti-apoptotic protein; NRH gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Aouacheria, A., Arnaud, E., Venet, S., Lalle, P., Gouy, M., Rigal, D. and
Gillet, G.
NRH, a human homologue of Nr-13 associates with Bcl-Xs and is an
TITLE

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JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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7 PASSAGE  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 95.48% Indels: 0  
DB: 9 Gaps: 0  
US-10-071-174-2 (1-204) x HSA458330 (1-585)  
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QY 31 AlaArgGluProGlyThrProGluProAlaProSerThrProGluAlaValLeuArg 50  
DB 61 GCCCGGAAACCCGACCCCGAGCGCGCCATCCACGCCGAGCGCGCTGCTGGCGC 120  
QY 51 SerAlaAlaAlaGluArgGlnIleHisArgSerPhePheSerAlaTyrLeuGlyTyr 70  
DB 121 TCCGCGCGCCGAGGTACGGCAGATTCACCGGTCTTTTCTCCGCTTACCTCGGCTAC 180  
QY 71 ProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerPro 90  
DB 181 CCGCGGAACCGCTTCGAGCTGTGGCGCTGATGGCGGATTCGCTCTCCGACAGCCCC 240  
QY 91 GlyProThrTrpGlyArgValThrLeuValThrPheAlaGlyThrLeuLeuGluArg 110  
DB 241 GCGCCACCTGGCGGAGAGTGTGACGCTCGTACCTTCGAGGACGCTGCTGGAGAGA 300  
QY 111 GlyProLeuValThrAlaArgTrpLysLysTyrPheGlnProArgLeuLysGluGln 130  
DB 301 GGGCCCTGTTGACCCCGCGGTGGAGAGTGGGCTTCACCGCGGCTAAGAGGAGCAG 360  
QY 131 GluGlyAspValAlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArgLeuVal 150  
DB 361 GAGGGCGAGCTGCGCCGGGACTGCCAGCGCTGGTGGCTTCTGAGCTCGCGGCTCATG 420  
QY 151 GlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrpAspGlyPheCysHisPhePhe 170  
DB 421 GGGCAGCAGCGCCCTGGCTGAGGGCTGAGGGCGCTGGGATGGCTTTTGTGCTTCTTC 480

QY 171 ArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCys 190  
DB 481 AGGACCCCTTTCCACTGGCTTTTGGAGAAACACAGCTGTCACAGCTTTCTGTATGC 540  
QY 191 LeuLeuThrThrAlaPheIleTyrLeuTrpThrArgLeuLeu 204  
DB 541 TTGTAAACACAGCTTCATTATCTCTGACACAGATTATTA 582  
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LOCUS AC023906 93287 bp DNA linear PRI 06-JUL-2001  
DEFINITION Homo sapiens chromosome 15 clone CTD-2184D3 map 15q21.2, complete  
sequence.  
AC023906  
ACCESSION AC023906  
VERSION AC023906.7 GI:14595770  
KEYWORDS HTC  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.  
TITLE Sequencing of human chromosome 15 D15S146-D15S117 region  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T. and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA  
REFERENCE 3 (bases 1 to 93287)  
AUTHORS Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA  
COMMENT On Jul 4, 2001 this sequence version replaced gi:12248292.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UWMSC  
Web site: http://chroma.mbt.washington.edu/msg\_www  
Contact: leerowens@systemsbiology.org  
----- Summary Statistics  
Sequencing vector: pUC18, L08752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
Note: Data from overlapping BACs AC010674 [drafting center: UWMSC], AC090970 [drafting center: UWMSC], and AC016824 [drafting center: GTC] was added for finishing  
----- Location/Qualifiers  
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54966 gap of unknown length  
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Alignment Scores:

Pred. No.: 1.96e-29 Length: 214669  
Score: 494.00 Matches: 110  
Percent Similarity: 77.63% Conservative: 8  
Best Local Similarity: 72.37% Mismatches: 33  
Query Match: 45.57% Indels: 2  
DB: 2 Gaps: 0

US-10-071-174-2 (1-204) x AC018903 (1-214669)

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Db 93362 ATGTTTGCACCTTTCGGGAGCGCCACCACCATGTGCGACCCGTCGCGAGCGACCGAG 93321  
Qy 21 LeuLeuLeuAlaAspTyrLeuGlyTyr-CysAlaArgGluProGlyThrProGluProAl 40  
Db 93322 CTGTGTCTGCCGACTACTAGACTCTCTCCCGGGAACCTCGCACCCCGAGCGGAG 93381

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Qy 40 aProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHi 60
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Qy 60 sArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLe 80
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Qy 80 uMetAlaAspSerValLeuSerAspSerProGlyProThrTyrGlyArgValValThrLe 100
Db 93502 GATGGCGATTCGTTACTCTCCACAGACCCGTCGCCACCTAGGCGGAAAGGAGCGCT 93561
Qy 100 uValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTyrLysLy 120
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Qy 120 sTyrGlyPheGlnProArgLeuLysGlnGlnGlyAspValAlaAlaArgAspCysGlnAr 140
Db 93622 AATAGCTTTCAACCCCGGTAAAGAACAAAGAGACACTCGGCCCA-GACTGCCAACA 93680
Qy 140 gLeuValAlaLeuSerSerArgLeuMetGly 151
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RESULT 9
AY029163 1074 bp mRNA linear ROD 19-JUN-2003
LOCUS Rattus norvegicus BCL2L10 (Bcl2l10) mRNA, complete cds.
DEFINITION Rattus norvegicus BCL2L10 (Bcl2l10) mRNA, complete cds.
ACCESSION AY029163
VERSION AY029163.1 GI:13641257
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 1074)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Bcl-2-related protein family gene expression during
Oligodendroglial differentiation
JOURNAL J. Neurochem. 85 (6), 1500-1512 (2003)
MEDLINE 22672518
PUBMED 12787069
REFERENCE 2 (bases 1 to 1074)
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-2001) Neurology Research, The Children's Hospital
of Philadelphia, Abramson Research Center, Room 516 I, 3517 Civic
Center Boulevard, Philadelphia, PA 19104, USA
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CDS 12. 569
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ORIGIN
Alignment Scores: 2.84e-31 Length: 1074
Pred. No.: 487.00 Matches: 89
Score:

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Percent Similarity: 64.58% Conservative: 35
Best Local Similarity: 46.35% Mismatches: 56
Query Match: 44.93% Indels: 12
DB: 10 Gaps: 2

US-10-071-174-2 (1-204) x AY029163 (1-1074)
Qy 11 MetAlaAspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeuGlyTyrCys 30
Db 12 ATGGGTGACCCGCTGCAGGATCGACTAGACGGCTGCTGACTGACTACATATTGTTCTGC 71
Qy 31 AlaArgGluProGlyThrProGluProAlaProSerThrProGluAlaAlaValLeuArg 50
Db 72 GCAGCGCGCGCAACCCCTGAGCCACTCCCGCTGCTGTTGAGCGGCGCTTGTGCGC 131
Qy 51 SerAlaAlaAlaArgLeuArgGlnIleHisArgSerPhePheSerAlaTyrLeuGlyTyr 70
Db 132 TCTGTGACTAGTCAGATCCCAACAGGACACAGGATCTTTTCAACTCCTTCGCGACTAC 191
Qy 71 ProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerPro 90
Db 192 CAGGCAACCGCCTGGAGCTGGTGACACAGATGCGGATGAGTTGCTCTCCAATGACCAA 251
Qy 91 GlyProThrTyrGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArg 110
Db 252 GAGTTCAACTGGGCGCCCTGGTGATGCTCTCGCTTCGTGGGAGCGCTAATGACCAA 311
Qy 111 GlyProLeuValThrAlaArgTyrLysLysTyrGlyPheGlnProArgLeuLysGluGln 130
Db 312 GACAGGACTGTTAAGCGGAGG-----AGGGATCAA 341
Qy 131 GluGlyAsp-----ValAlaArgAspCysGlnArgLeuValAlaLeuSerSerArg 148
Db 342 AGAAACCGTCTCTACTGAGCGAGACTGCTATCTCATAGTGAGCTGCTGTACATCGA 401
Qy 149 LeuMetGlyGlnHisArgAlaTyrLeuGlnAlaGlnGlyTyrAspGlyPheCysHis 168
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Qy 169 PhePheArgThrProPheProLeuAlaPheTyrArgLysGlnLeuValGlnAlaPheLeu 198
Db 462 TTCTTCAAGAACCCCTTACCACCGCGCTTCTGAGAAGATTGCTGATCCGGGCTATTCTG 521
Qy 189 SerCysLeuLeuThrThrAlaPheIleTyrLeuTyr 200
Db 522 TCCGTGTTCTTGCACGCGCATCTTTATATCTGG 557

RESULT 10
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LOCUS Mus musculus Bcl-2 homolog (Boo) mRNA, complete cds.
DEFINITION Mus musculus Bcl-2 homolog (Boo) mRNA, complete cds.
ACCESSION AF102501
VERSION AF102501.1 GI:4165137
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1209)
AUTHORS Song,Q., Kuang,Y., Dixit,V.M. and Vincenz,C.
TITLE Boo, a novel negative regulator of cell death, interacts with
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL EMBO J. 18 (1), 167-178 (1999)
MEDLINE 99094902
PUBMED 9878060
REFERENCE 2 (bases 1 to 1209)
AUTHORS Song,Q.Z., Kuang,Y.P., Dixit,V.M. and Vincenz,C.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) Pathology, University of Michigan, 1301
Catherine Road, Ann Arbor, MI 48109, USA
FEATURES
source 1. 1209
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Score: 474.50 Matches: 94
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Query Match: 43.77% Indels: 13
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US-10-071-174-2 (1-204) x AF102501 (1-1209)
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Db 132 GACCCACTGCATGACGCACCTAGACGGCTGCTGCTGACTACATATCTTCGCGCAGG 191
QY 33 GluProGlyThrProGluProAlaProSerThrProGluAlaAlaValLeuArgSerAla 52
Db 192 GAGCGGACACCCAGAGCACCGCCACGCTGCTGAGCGCGCTTGCTCGCTCTGTG 251
QY 53 AlaAlaArgLeuArgGlnIleHisArgSerPheSerAlaTyrLeuGlyTyrProGly 72
Db 252 ACTAGGCATGATCAGCAGGACCAAGAAATTTTTCCTCTCTGCGAAAGCGGGCG 311
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Db 312 AATCGCCTGGAGCTGGTGAACAGATGGCAGATAGTTGCTCTCCAAAGACCAAGACTC 371
QY 93 ThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArgGlyPro 112
Db 372 AGCTGGAGCAACTGGTGATGCTCTGCGCTTCGCGGAGCGCTTATGAATCAAGCCCT 431
QY 113 LeuValThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGlnGly 132
Db 432 TACATGGCTGTCAAGCAGAGAGG-----GATCTGGG 464
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QY 150 MetGly---GlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrpAspGlyPheCysHis 168
Db 525 ATGGGCGCTGGCAGCCGCGCAGCTGGAGGCTCTCGCGCGCTGGAGTGGCTTTTGGCGG 584
QY 169 PhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeu 188
Db 585 TTCTTCAAGAAATCTTTACCGCTCGGCTTCTGGAGAAGATTCGTGATTCAGGCTTTCTG 644
QY 189 SerCysLeuLeuThrThrAlaPheIleTyrLeuTrpThrArgLeu 203
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RESULT 11

AF067660

LOCUS

AF067660 1225 bp mRNA linear ROD 04-DEC-1998

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DEFINITION Mus musculus Bcl-2 homolog (Diva) mRNA, complete cds.
ACCESSION AF067660
VERSION AF067660.1 GI:3955265
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1225)
AUTHORS Inohara,N., Gourley,T.S., Carrio,R., Muniz,M., Merino,J.,
Garcia,I., Koseki,T., Hu,Y., Chen,S. and Nunez,G.
TITLE Diva, a Bcl-2 homologue that binds directly to Apaf-1 and induces
BH3-independent cell death
JOURNAL J. Biol. Chem. 273 (49), 32479-32486 (1998)
MEDLINE 99047617
PUBMED 9829980
REFERENCE 2 (bases 1 to 1225)
AUTHORS Inohara,N. and Nunez,G.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-1998) Department of Pathology, University of
Michigan Medical School, 1500 E. Medical Dr., Ann Arbor, MI 48109,
USA
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Best Local Similarity: 48.21% Mismatches: 56
Query Match: 43.77% Indels: 13
DB: 10 Gaps: 3
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QY 13 AspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeuGlyTyrCysAlaArg 32
Db 158 GACCCACTGCATGACGCACCTAGACGGCTGCTGCTGACTACATATCTTCGCGCAGG 217
QY 33 GluProGlyThrProGluProAlaProSerThrProGluAlaAlaValLeuArgSerAla 52
Db 218 GAGCGGACACCCAGAGCACCGCCACGCTGCTGAGCGCGCTTGCTCTGCTGTG 277
QY 53 AlaAlaArgLeuArgGlnIleHisArgSerPheSerAlaTyrLeuGlyTyrProGly 72
Db 278 ACTAGGCATGATCAGCAGGACCAAGAAATTTTTCCTCTCTGCGAAAGCGGGCG 337
QY 73 AsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerProGlyPro 92
Db 338 AATCGCCTGGAGCTGGTGAACAGATGGCAGATAAGTTGCTCTCCAAAGACCAAGACTTC 397

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QY 93 ThrTTPGlyArgValThrLeuValThrPheAlaGlyThrLeuLeuGluArgGlyPro 112  
 Db 398 AGCTGAGGCAACTGCTGATGCTCTGGCCCTTCGGGGAGCCTTATGAATCAAGGCCCT 457  
 QY 113 LeuValThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGlnGly 132  
 Db 458 TACATGGCTGTCAAGCAGAGAGG-----GATCTGGGG 490  
 QY 133 Asp-----ValAlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArgLeu 149  
 Db 491 AATCGTGTATAGTACCGCAGACTGCTGCTCATAGTGAATTTCTGTATAATATGCTC 550  
 QY 150 MetGly---GlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrpAspGlyPheCysHis 168  
 Db 551 ATGGGGCTGTCGGCACCAGCCAGGCTGGAGGCTCTCGGGCGCTGGATGGCTTTGCCGC 610  
 QY 169 PhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeu 188  
 Db 611 TTCTTCAAGAAATCTTTACCGCTCGCTTCTGGAGAAGATTGCTGATTGAGCCTTTCTG 670  
 QY 189 SerCysLeuLeuThrThrAlaPheLeuTyrLeuTyrThrArgLeu 203  
 Db 671 TCAGGCTTCTTGCACAGCAGCATCTTTTATCTGGAACAGTTA 715

RESULT 12  
 BC052690 1257 bp mRNA linear ROD 08-OCT-2003  
 LOCUS Mus musculus Bcl2-like 10, mRNA (cDNA clone MGC:60542  
 DEFINITION IMAGE:30052580), complete cds.

ACCESSION BC052690  
 VERSION BC052690.1 GI:30851238  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 1257)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Heiton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 22388257  
 12477932

## REFERENCE

2 (bases 1 to 1257)  
 Strausberg, R.

## AUTHORS

Direct Submission  
 Submitted (16-MAY-2003) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgaps-x@mail.nih.gov](mailto:cgaps-x@mail.nih.gov)

Tissue Procurement: Minoru Ko

cDNA Library Preparation: Yulan Piao and Minoru Ko (National

Institute on Aging, NIH: <http://lgeun.grc.nia.nih.gov/cDNA/>)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mgc@hghri.nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Loric, P., Legaapi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,  
 Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 112 Row: h Column: 18  
 This clone was selected for full length sequencing because it  
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## ORIGIN

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 Percent Similarity: 64.10% Conservative: 32  
 Best Local Similarity: 47.69% Mismatches: 57  
 Query Match: 43.13% Indels: 13  
 DB: 10 Gaps: 3

US-10-071-174-2 (1-204) x BC052690 (1-1257)

QY 13 AspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeuGlyTyrCysAlaArg 32  
 Db 160 GACCACTGATGACCGACCTAGACGGCTGCTGTGACTACATATTTCTCGGCACGG 219  
 QY 33 GluProGlyThrProGluProAlaProSerThrProGluAlaAlaValLeuArgSerAla 52  
 Db 220 GAGCGGACACCCCGAGAGCCCGCCACCTCTGTGCGCGCGCTTGTCTCTGTG 279



\* as soon as it is available and the accession number will  
\* be preserved.

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9893 118024: contig of 108132 bp in length  
118025 118124: gap of unknown length  
118125 236958: contig of 118334 bp in length  
236959 237058: gap of unknown length  
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Query Match: 31.55% Indels: 13  
DB: 2 Gaps: 2

US-10-071-174-2 (1-204) x AC111669 (1-240461)

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Db 21870 GCAGGCGCGGACACCCCTGAGCCACTGCCACGCTCTGTTGAGCGCGCTTGTCTGC 21929  
Qy 50 gSerAlaAlaArgLeuArgGlnIleHisArgSerPhePheSerAlaTyrLeuGlyTy 70  
Db 21930 CTCTGTGACTAGTCAGATCCACAGGAGCACCAGGATCTTTTCACTCTCTCGGACTA 21989  
Qy 70 rProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerPr 90  
Db 21990 CCAGGCGACCGCTGAGCTGTGTGACAGATGGCGGATGCTCTCCATGACCA 22049  
Qy 90 oGlyProThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluAr 110  
Db 22050 AGAGTTCAACTGGCGCGCTGTGTGATGCTCTCGGCTTCTGTGGGACGCTAATGAACCA 22109  
Qy 110 gGlyProLeuValThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGl 130  
Db 22110 AGACAGACTGTTAAGCGGAGG-----AGGATCA 22139  
Qy 130 nGluGlyAsp-----ValAlaArgAspCysGlnArgLeuValAlaLeuSerSerAr 148  
Db 22140 AAGAAACCGTCTCTACTGAGCGAGACTGCTATCTCATAGTAGCTTGTGTACAATCG 22199  
Qy 148 gLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrp 163  
Db 22200 ACTCACAGGACGGCATCGCTCTGCTGGTGGAGGCTCACGGCTGGCTGG 22245

## RESULT 14

AC133947

## LOCUS

DEFINITION  
Mus musculus chromosome 9 clone RP24-18912, WORKING DRAFT SEQUENCE,  
3 unordered pieces.

## ACCESSION

AC133947

## VERSION

AC133947.2 GI:50199129

## KEYWORDS

HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 169914)

## AUTHORS

Wilson, R.K.

## TITLE

The sequence of Mus musculus clone

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 169914)

## AUTHORS

McPherson, J.D. and Waterston, R.H.

## TITLE

Direct Submission

## JOURNAL

Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA

## REFERENCE

3 (bases 1 to 169914)

## AUTHORS

Wilson, R.K.

## TITLE

Direct Submission

## JOURNAL

Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA

## COMMENT

On Jul 10, 2004 this sequence version replaced gi:23238076.

AC133947 169914 bp DNA linear HTG 10-JUL-2004  
Mus musculus chromosome 9 clone RP24-18912, WORKING DRAFT SEQUENCE,  
3 unordered pieces.

AC133947  
AC133947.2 GI:50199129  
HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 169914)

Wilson, R.K.  
The sequence of Mus musculus clone  
Unpublished

McPherson, J.D. and Waterston, R.H.  
Direct Submission  
Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 169914)  
Wilson, R.K.  
Direct Submission

Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA

On Jul 10, 2004 this sequence version replaced gi:23238076.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu

Contact: submissions@wustl.edu

----- Project Information -----

Center project name: M\_BB0189102

----- Summary Statistics -----

Sequencing vector: M13; 0%

Sequencing method: plasmid; 100%

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 167792 bases at least Q40

Consensus quality: 168148 bases at least Q30

Consensus quality: 168291 bases at least Q20

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 21204: contig of 21204 bp in length  
\* 21205 21304: gap of unknown length  
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misc\_feature

misc\_feature





Job time : 4754 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 21:41:06 ; Search time 6234 Seconds  
(without alignments)  
6728.579 Million cell updates/sec

Title: US-10-071-174-1  
Perfect score: 887  
Sequence: 1 cgggccaagaaccagcga.....ctcttccttgactgaagaa 887

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	887	100.0	887	9	AF326964	AF326964 Homo sapi
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3	615	69.3	615	9	AF285052	AF285052 Homo sapi
4	585	66.0	585	9	HSA458330	AJ458330 Homo sapi
5	582	65.6	582	6	BD233456	BD233456 Human pro
6	574.4	64.8	726	6	CQ752105	CQ752105 Sequence
7	539.2	60.8	93287	9	AC023906	AC023906 Homo sapi
8	345.6	39.0	214659	2	AC018903	AC018903 Homo sapi
9	327.5	36.9	214659	2	AC018903	AC018903 Homo sapi
10	259.2	29.2	1229	10	AF102501	AF102501 Mus muscu
11	259.2	29.2	1225	10	AF067660	AF067660 Mus muscu
12	257.6	29.0	1257	10	BC052690	BC052690 Mus muscu
13	244.2	27.5	1074	10	AY029163	AY029163 Rattus no
14	147	16.6	169914	2	AC133947	AC133947 Mus muscu
15	147	16.6	202851	2	AC115880	AC115880 Mus muscu
16	141.8	16.0	240451	2	AC111659	AC111659 Rattus no
17	95.4	10.8	243686	2	AC036430	AC036430 Rattus no
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C 20	62.2	7.0	295150	1	SC0939126	AL939126 Streptomy
C 21	61.2	6.9	125020	9	AF429315	AF429315 Homo sapi
C 22	60	6.8	60	6	CQ545914	CQ545914 Sequence
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C 24	58.2	6.6	125020	9	AF429315	AF429315 Homo sapi
C 25	57.4	6.5	82746	1	AF453501	AF453501 Actinosyn
C 26	57.2	6.4	3987	9	BC036533	BC036533 Homo sapi
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C 28	57	6.4	1822	5	GCCHX14	Y16952 Amycolatops
C 29	56.8	6.4	66669	1	AME16952	AL939106 Streptomy
C 30	56.8	6.4	314100	1	SC0939106	AL939106 Streptomy
C 31	56.4	6.4	963	11	PM12H123	AB04456 Penicilli
C 32	55.6	6.3	943	9	AB042637S3	AB042637 Homo sapi
C 33	55.6	6.3	2507	9	AB042636	AB042636 Homo sapi
C 34	55.6	6.3	2811	9	AX055486	AX055486 Homo sapi
C 35	55.6	6.3	4023	9	AK126663	AK126663 Homo sapi
C 36	55.6	6.3	97110	2	AC016815	AC016815 Homo sapi
C 37	55.6	6.3	137960	2	AC103889	AC103889 Homo sapi
C 38	55.6	6.3	168133	2	AC093622	AC093622 Homo sapi
C 39	55.6	6.3	208236	9	AC010536	AC010536 Homo sapi
C 40	55.2	6.2	1265	8	AK108845	AK108845 Oryza sat
C 41	55.2	6.2	2997	6	AX552616	AX552616 Sequence
C 42	55.2	6.2	3158	6	AX552614	AX552614 Sequence
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C 44	55.2	6.2	140142	8	AP005871	AP005871 Oryza sat
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ALIGNMENTS

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Homo sapiens BCLB (BCLB) mRNA, complete cds.  
AF326964.1 GI:13898393  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
21201065  
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2 (bases 1 to 887)  
Ke.N., Godzik,A. and Reed,J.C.  
Bcl-2, a novel Bcl-2 family member that differentially binds and  
regulates Bax and Bak  
J. Biol. Chem. 276 (16), 12481-12484 (2001)  
21201065  
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2 (bases 1 to 887)  
Ke.N., Godzik,A. and Reed,J.C.  
Direct Submission  
Submitted (07-DEC-2000) The Burnham Institute, 10901 N. Torrey  
Pines Rd., La Jolla, CA 92037, USA  
JOURNAL  
Pines Rd., La Jolla, CA 92037, USA  
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ORIGIN

Query Match 100.0%; Score 887; DB 9; Length 887;  
Best Local Similarity 100.0%; Pred. No. 5.4e-144;  
Matches 887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 CGTGCTCTCGGACAGCCCGCGCCCGCCAGCTGGGCGAGAGTGTGACGCTCGTGACCTTCG 360

Qy 361 AGGAGCGCTGTGAGAGAGCGCGCTGTGTGACCGCGCGGTGGAAGTGGGGCTTCCA 420  
Db 361 AGGAGCGCTGTGAGAGAGCGCGCTGTGTGACCGCGCGGTGGAAGTGGGGCTTCCA 420

Qy 421 GCCCGCGCTAAAGAGAGAGGAGCGGACGTCGCGCCCGGAGTGCAGCGCTGTGGCGCTT 480  
Db 421 GCCCGCGCTAAAGAGAGAGGAGCGGACGTCGCGCCCGGAGTGCAGCGCTGTGGCGCTT 480

Qy 481 GCTGAGCTCGGCGCTCATGCGGAGGAGCCCGCGCTGTGAGGCTCAGGCGGCTGGGA 540  
Db 481 GCTGAGCTCGGCGCTCATGCGGAGGAGCCCGCGCTGTGAGGCTCAGGCGGCTGGGA 540

Qy 541 TGGCTTTTGTCACTTCTTCAAGGACCCCTTTTCACTGGCTTTTGGAGAAACAGCTGCT 600  
Db 541 TGGCTTTTGTCACTTCTTCAAGGACCCCTTTTCACTGGCTTTTGGAGAAACAGCTGCT 600

Qy 601 CCAGGCTTTTCTGTCACTGTGTTAAACAGAGCTTCAATTTATCTTGACACGATTATT 660  
Db 601 CCAGGCTTTTCTGTCACTGTGTTAAACAGAGCTTCAATTTATCTTGACACGATTATT 660

Qy 661 ATGAGTTTAAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 720  
Db 661 ATGAGTTTAAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 720

Qy 721 ATGAGTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTT 780  
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Qy 781 ATGATACAGAGGAGTCTGAGGTTGTTGATTTGGCGAGTGTGTTAACTTGACAGTACT 840  
Db 781 ATGATACAGAGGAGTCTGAGGTTGTTGATTTGGCGAGTGTGTTAACTTGACAGTACT 840

Qy 841 CAGGTGTGAGGACAAAGAACTGAGGAAAGACCTTCCCGACCCCGACAGCTTTTATCTGA 887  
Db 841 CAGGTGTGAGGACAAAGAACTGAGGAAAGACCTTCCCGACCCCGACAGCTTTTATCTGA 887

RESULT 2  
BD233466  
LOCUS  
DEFINITION Human protein having hydrophobic domain and DNA encoding the same.  
ACCESSION BD233466

BD233466.1 GI:33043236  
JP 2002519016-A/12.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1168)  
AUTHORS Kato, S. and Kimura, T.  
TITLE Human protein having hydrophobic domain and DNA encoding the same  
JOURNAL Patent: JP 2002519016-A 12 02-JUL-2002;  
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC  
COMMENT CS Homo sapiens (human)  
PN JP 2002519016-A/12  
PD 02-JUL-2002  
PF 18-JUN-1999 JP 2000557267  
PI SEISHI KATO, TOMOKO KIMURA  
PC  
C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N5/00, C12N5/ PC  
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CC Human protein having hydrophobic domain and DNA encoding the  
CC same  
FH Key 1..1168 Location/Qualifiers  
FT source /organism="Homo sapiens (human)";  
FEATURES  
source 1..1168 Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 91.6%; Score 812.4; DB 6; Length 1168;  
Best Local Similarity 99.9%; Pred. No. 4.5e-131;  
Matches 813; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 74 ACCACCATGGCCGACCGCTGCGGAGCGGACCGAGCTGTGTGGCGGACCTACCTGGGG 133  
Db 1 ACCACCATGGCCGACCGCTGCGGAGCGGACCGAGCTGTGTGGCGGACCTACCTGGGG 60

Qy 134 TACTGCGCGCGGGAACCGGCAACCCCGAGCGCGGCATCCAGCCCGAGGCGCGCGTG 193  
Db 61 TACTGCGCGCGGGAACCGGCAACCCCGAGCGCGGCATCCAGCCCGAGGCGCGCGTG 120

Qy 194 CTGCGCTCCGCGCGCGCGGACGCTTACGCGAGATTACCGGCTCTTTTCTCCGCTACCTC 253  
Db 121 CTGCGCTCCGCGCGCGCGGACGCTTACGCGAGATTACCGGCTCTTTTCTCCGCTACCTC 180

Qy 254 GGCTACCGCGGGAACCGCTTTCGAGCTGTGGCGTGTGCGGATTCGCTCTCCGAC 313  
Db 181 GGCTACCGCGGGAACCGCTTTCGAGCTGTGGCGTGTGCGGATTCGCTCTCCGAC 240

Qy 314 AGCCCGCGCGCCACCTGGGCGAGAGTGTGACGCTCGTGACCTTCGAGGAGCGCTCTG 373  
Db 241 AGCCCGCGCGCCACCTGGGCGAGAGTGTGACGCTCGTGACCTTCGAGGAGCGCTCTG 300

Qy 374 GAGAGAGGCGCGCTGTGTGACCGCCCGGTGGAAGTGGGGCTTCAGCCCGGCTAAAG 433  
Db 301 GAGAGAGGCGCGCTGTGTGACCGCCCGGTGGAAGTGGGGCTTCAGCCCGGCTAAAG 360

Qy 434 GAGCAGAGGCGGACGCTGCGCCGGGACTGCGAGCGCTGTGGCTTCGCTGAGCTCCGG 493  
Db 361 GAGCAGAGGCGGACGCTGCGCCGGGACTGCGAGCGCTGTGGCTTCGCTGAGCTCCGG 420

Qy 494 CTCATGGGCGGACCGCGCTGCTGAGGCTCAGGCGCGCTGGGATGCTTTTGTAC 553  
Db 421 CTCATGGGCGGACCGCGCTGCTGAGGCTCAGGCGCGCTGGGATGCTTTTGTAC 480

Qy 554 TTCCTCAGGACCCCTTTTCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTG 613  
Db 481 TTCCTCAGGACCCCTTTTCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTG 540

Qy 614 TCATGCTGTTTAAACACAGCGCTTCATTATCTCTGGACAGCATTTATGAGTTTAAAA 673

Db 541 TCATGCTGTGTTAAACACACGCTTCATTTATCTCTGGACACGATTATTATGATTTTAAAA 600  
QY 674 CTTTAAACCGGCTTTCACCTGCGCCAACTGTGACCACTAAATGACAGATGTGTGAGAACA 733  
Db 601 CTTTAAACCGGCTTTCACCTGCGCCAACTGTGACCACTAAATGACAGATGTGTGAGAACA 660  
QY 734 AGAATGAGGGAAGAACACCTTCCCAACCCAGAGAGTCTTTTATCTGAATGATCAAGGA 793  
Db 661 AGAATGAGGGAAGAACACCTTCCCAACCCAGAGAGTCTTTTATCTGAATGATCAAGGA 720  
QY 794 GTCTCTGAGTGTGGTGAATTTGGCCAGTGTCTTAACTTGTGACAAAGTACTCAGGTGTGAGGAC 853  
Db 721 GTCTCTGAGTGTGGTGAATTTGGCCAGTGTCTTAACTTGTGACAAAGTACTCAGGTGTGAGGAC 780  
QY 854 AGAATGCAAAATGGCTCTTCCTTGAGTGAAGAA 887  
Db 781 AGAATGCAAAATGGCTCTTCCTTGAGTGAAGAA 814

RESULT 3  
AF285092 615 bp mRNA linear PRI 08-NOV-2001  
LOCUS Homo sapiens Bcl-2-like protein 10 mRNA, complete cds.  
DEFINITION  
ACCESSION AF285092  
VERSION AF285092.1 GI:9837265

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 615)  
AUTHORS Zhang, H., Holzgreve, W. and De Geyter, C.  
TITLE Bcl2-L-10, a novel anti-apoptotic member of the Bcl-2 family, blocks apoptosis in the mitochondria death pathway but not in the death receptor pathway

JOURNAL Hum. Mol. Genet. 10 (21), 2329-2339 (2001)  
MEDLINE 21548034  
PUBMED 11689480  
REFERENCE 2 (bases 1 to 615)  
AUTHORS Zhang, H.H.  
TITLE Direct Submission  
JOURNAL Submitted (05-JUL-2000) University Women's Hospital, Schanzenstra 46, Basel 4057, Switzerland

FEATURES  
source Location/Qualifiers  
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GWDGCFHFRRFPFLAFWRKQLVQAFISCLLTATFIVLTLL"

ORIGIN  
Query Match 69.3%; Score 615; DB 9; Length 615;  
Best Local Similarity 100.0%; Pred. No. 8e-97;  
Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 50 ATGGTTGACAGTTGGGGAGCGCACCCACCATGGCCGCTCGGGAGCGCACCGAG 109  
Db 1 ATGGTTGACAGTTGGGGAGCGCACCCACCATGGCCGCTCGGGAGCGCACCGAG 60  
QY 110 CTGTTCTGGCCGACTACTGGGGTACTCGCCCGGGAAACCCGGACCCCGAGCCGCG 169  
Db 61 CTGTTCTGGCCGACTACTGGGGTACTCGCCCGGGAAACCCGGACCCCGAGCCGCG 120

QY 170 CCATCCACGCCGAGGCCGCGTGTCTCGCTCCGCGCCGCGCCAGGTTACGGCAGATTAC 229  
Db 121 CCATCCACGCCGAGGCCGCGTGTCTCGCTCCGCGCCGCGCCAGGTTACGGCAGATTAC 180  
QY 230 CGGTCTCTTTTCTCCGCTACTCTCGGTACCCCGGAGACCGCTTCGAGCTGGTGGGCTG 289  
Db 181 CGGTCTCTTTTCTCCGCTACTCTCGGTACCCCGGAGACCGCTTCGAGCTGGTGGGCTG 240  
QY 290 ATGGCGGATTCGGTCTCTCCGACAGCCCGCGCCACCTTGGGGCAGAGTGGTGACGCTC 349  
Db 241 ATGGCGGATTCGGTCTCTCCGACAGCCCGCGCCACCTTGGGGCAGAGTGGTGACGCTC 300  
QY 350 GTGACCTTCGAGGAGACGCTGTGTGAGAGAGGCGCTGTGTGACCCGCCCGTGAAGAAG 409  
Db 301 GTGACCTTCGAGGAGACGCTGTGTGAGAGAGGCGCTGTGTGACCCGCCCGTGAAGAAG 360  
QY 410 TGGGGCTTCAGCGCGCTAAAGGAGCAGAGGAGCGCTCGCCCGGGACTGCCAGCGC 469  
Db 361 TGGGGCTTCAGCGCGCTAAAGGAGCAGAGGAGCGCTCGCCCGGGACTGCCAGCGC 420  
QY 470 CTGTGCGCTTGTGAGCTCGCGCTCATGGGAGCAGCACCGCGCTGGTGCAGGCTCAG 529  
Db 421 CTGTGCGCTTGTGAGCTCGCGCTCATGGGAGCAGCACCGCGCTGGTGCAGGCTCAG 480  
QY 530 GGCGGCTGGGATGGCTTTTGTCTCTCTTTCAGGACCCCTTTCACCTGGCTTTTGAGA 589  
Db 481 GGCGGCTGGGATGGCTTTTGTCTCTTTCAGGACCCCTTTCACCTGGCTTTTGAGA 540  
QY 590 AAACAGCTGTGCCAGGCTTTTCTGTCTGTGTGTTTAAACACAGCCTTCAATTTATCTGG 649  
Db 541 AAACAGCTGTGCCAGGCTTTTCTGTCTGTGTGTTTAAACACAGCCTTCAATTTATCTGG 600  
QY 650 ACAGGATTATATGA 664  
Db 601 ACAGGATTATATGA 615

RESULT 4  
HSA458330 585 bp DNA linear PRI 25-APR-2002  
LOCUS Homo sapiens NRH gene for anti-apoptotic protein.  
DEFINITION  
ACCESSION AJ458330  
VERSION AJ458330.1 GI:20338765  
KEYWORDS anti-apoptotic protein; NRH gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
AUTHORS Aouacheria, A., Arnaud, E., Venet, S., Lalle, P., Gouy, M., Rigal, D. and Gillet, G.  
TITLE Nrh, a human homologue of Nr-13 associates with Bcl-Xs and is an inhibitor of apoptosis  
JOURNAL Oncogene 20 (41), 5846-5855 (2001)  
MEDLINE 21477277  
PUBMED 11593390  
REFERENCE 2 (bases 1 to 585)  
AUTHORS Gillet, G.  
TITLE Direct Submission  
JOURNAL Submitted (23-APR-2002) Gillet G., Ibcop, CNRS UMR 5086, 7 PASSAGE DU VERCORS, 69367, FRANCE

FEATURES  
source Location/Qualifiers  
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 /db\_xref="GI:20338766"  
 /db\_xref="GOA:Q9HD36"  
 /db\_xref="Swiss-Prot:Q9HD36"  
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 RTPFLAFWRKQLVQAFSLCLLTATTAFLVLTLL"

## ORIGIN

Query Match 66.0%; Score 585; DB 9; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-91;  
 Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ATGCGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGCGCGACTACCTGGGGTACTGC 139  
 Db 1 ATGCGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGCGCGACTACCTGGGGTACTGC 60

QY 140 GCCCGGGAACCCCGGACCCCGGAGCGCGCCATCCACGCCGAGCGCCGCTGTGCGC 199  
 Db 61 GCCCGGGAACCCCGGACCCCGGAGCGCGCCATCCACGCCGAGCGCCGCTGTGCGC 120

QY 200 TCGCGCGCGCCAGGTTACGGAGATTACCGGTCCTTTTCTCGCGCTACCTCGGCTAC 259  
 Db 121 TCGCGCGCGCCAGGTTACGGAGATTACCGGTCCTTTTCTCGCGCTACCTCGGCTAC 180

QY 260 CCCCGGAACCCGCTTCGAGCTGTGGCGCTGATGGCGGATTCGCTGCTCCGACAGCCGC 319  
 Db 181 CCCCGGAACCCGCTTCGAGCTGTGGCGCTGATGGCGGATTCGCTGCTCCGACAGCCGC 240

QY 320 GCGCCACCTGCGGAGAGTGTGAGCTCGTACCTTCGAGGAGCGCTGCTGGAGAGA 379  
 Db 241 GCGCCACCTGCGGAGAGTGTGAGCTCGTACCTTCGAGGAGCGCTGCTGGAGAGA 300

QY 380 GGGCGCTGTGTACCGCCCGGCTGGAAGAGTGGGGCTTCACGCCGGCTAAAGGAGCAG 439  
 Db 301 GGGCGCTGTGTACCGCCCGGCTGGAAGAGTGGGGCTTCACGCCGGCTAAAGGAGCAG 360

QY 440 GAGGCGAGCTCGCCGGGACTCCAGCGCTGGTGGCTTCTGAGCTCGCGGCTCATG 499  
 Db 361 GAGGCGAGCTCGCCGGGACTCCAGCGCTGGTGGCTTCTGAGCTCGCGGCTCATG 420

QY 500 GGGCAGCACCAGCCCTGGCTGAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTC 559  
 Db 421 GGGCAGCACCAGCCCTGGCTGAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTC 480

QY 560 AGGACCCCTTTCAGTGGCTTTTGGAGAAACAGCTGGTCCAGCTTTTCTGTCATGC 619  
 Db 481 AGGACCCCTTTCAGTGGCTTTTGGAGAAACAGCTGGTCCAGCTTTTCTGTCATGC 540

QY 620 TTGTTAAACAACAGCTTCATTATCTCTGGACACGATTATTATGA 664  
 Db 541 TTGTTAAACAACAGCTTCATTATCTCTGGACACGATTATTATGA 585

RESULT 5  
 BD233456  
 LOCUS 582 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Human protein having hydrophobic domain and DNA encoding the same.  
 ACCESSION BD233456  
 VERSION BD233456.1 GI:33043226  
 KEYWORDS JP 2002519016-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 582)  
 Kato, S. and Kimura, T.  
 Human protein having hydrophobic domain and DNA encoding the same  
 Patent: JP 2002519016-A 2 02-JUL-2002;  
 SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

COMMENT OS Homo sapiens (human)  
 PN JP 2002519016-A/2  
 PD 02-JUL-2002  
 PF 18-JUN-1999 PF 2000557267  
 PI SEISHI KATO, TOMOKO KIMURA  
 PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N15/00, C12N5/ PC  
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 CC Human protein having hydrophobic domain and DNA encoding the  
 CC same  
 FH Key Location/Qualifiers  
 FT source 1..582 /organism="Homo sapiens (human)".  
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 source Location/Qualifiers  
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ORIGIN

Query Match 65.6%; Score 582; DB 6; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-91;  
 Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ATGCGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGCGCGACTACCTGGGGTACTGC 139  
 Db 1 ATGCGCGACCCGCTGCGGAGCGCACCGAGCTGTGCTGCGCGACTACCTGGGGTACTGC 60

QY 140 GCCCGGGAACCCCGGACCCCGGAGCGCGCCATCCACGCCGAGCGCCGCTGTGCGC 199  
 Db 61 GCCCGGGAACCCCGGACCCCGGAGCGCGCCATCCACGCCGAGCGCCGCTGTGCGC 120

QY 200 TCGCGCGCGCCAGGTTACGGAGATTACCGGTCCTTTTCTCGCGCTACCTCGGCTAC 259  
 Db 121 TCGCGCGCGCCAGGTTACGGAGATTACCGGTCCTTTTCTCGCGCTACCTCGGCTAC 180

QY 260 CCCCGGAACCCGCTTCGAGCTGTGGCGCTGATGGCGGATTCGCTGCTCCGACAGCCGC 319  
 Db 181 CCCCGGAACCCGCTTCGAGCTGTGGCGCTGATGGCGGATTCGCTGCTCCGACAGCCGC 240

QY 320 GCGCCACCTGCGGAGAGTGTGAGCTCGTACCTTCGAGGAGCGCTGCTGGAGAGA 379  
 Db 241 GCGCCACCTGCGGAGAGTGTGAGCTCGTACCTTCGAGGAGCGCTGCTGGAGAGA 300

QY 380 GGGCGCTGTGTACCGCCCGGCTGGAAGAGTGGGGCTTCACGCCGGCTAAAGGAGCAG 439  
 Db 301 GGGCGCTGTGTACCGCCCGGCTGGAAGAGTGGGGCTTCACGCCGGCTAAAGGAGCAG 360

QY 440 GAGGCGAGCTCGCCGGGACTCCAGCGCTGGTGGCTTCTGAGCTCGCGGCTCATG 499  
 Db 361 GAGGCGAGCTCGCCGGGACTCCAGCGCTGGTGGCTTCTGAGCTCGCGGCTCATG 420

QY 500 GGGCAGCACCAGCCCTGGCTGAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTC 559  
 Db 421 GGGCAGCACCAGCCCTGGCTGAGGCTCAGGGCGGCTGGGATGGCTTTTGTCACTTCTC 480

QY 560 AGGACCCCTTTCAGTGGCTTTTGGAGAAACAGCTGGTCCAGCTTTTCTGTCATGC 619  
 Db 481 AGGACCCCTTTCAGTGGCTTTTGGAGAAACAGCTGGTCCAGCTTTTCTGTCATGC 540

QY 620 TTGTTAAACAACAGCTTCATTATCTCTGGACACGATTATTATTA 661  
 Db 541 TTGTTAAACAACAGCTTCATTATCTCTGGACACGATTATTATTA 582

RESULT 6  
 CO752105  
 LOCUS 726 bp DNA linear PAT 03-FEB-2004  
 DEFINITION Sequence 38039 from Patent WO02068579.  
 ACCESSION CO752105  
 VERSION CO752105.1 GI:42387450  
 KEYWORDS Homo sapiens (human)  
 SOURCE

ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W.									
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof									
JOURNAL	Patent: WO 02068579-A 38039 06-SEP-2002; PE Corporation (NY) (US)									
FEATURES	Location/Qualifiers									
Source	1..726									
ORIGIN	/organism="Homo sapiens"									
	/mol_type="unassigned DNA"									
	/db_xref="taxon:9606"									
Query Match	64.8%; Score 574.4; DB 6; Length 726;									
Best Local Similarity	90.2%; Pred. No. 8,6e-90;									
Matches 655; Conservative	0; Mismatches 1; Indels 70; Gaps 1;									
QY	50	ATGTTGACAGTTCGGGAGCGACACACATGGCGGACCGCTCGGGAGCGCACCGAG	109							
Db	1	ATGTTGACAGTTCGGGAGCGACACACATGGCGGACCGCTCGGGAGCGCACCGAG	60							
QY	110	CTGTTGCTGGCGGACTACCTGGGTACTGCGCCCGGGAACCGGACCCCGAGCGCGC	169							
Db	61	CGTTGCTGGCGGACTACCTGGGTACTGCGCCCGGGAACCGGACCCCGAGCGCGC	120							
QY	170	CCATCCACCCCGAGCGCGCTGCTGCGCTCGCGGCGCCAGCTTACGGCAGATTCCAC	229							
Db	121	CCATCCACCCCGAGCGCGCTGCTGCGCTCGCGGCGCCAGCTTACGGCAGATTCCAC	180							
QY	230	CGGTCTCTTTTCTCGGCTACTCGGTACCCCGGGAACCGTTCGAGTGTGGCGTGT	289							
Db	181	CGGTCTCTTTTCTCGGCTACTCGGTACCCCGGGAACCGTTCGAGTGTGGCGTGT	240							
QY	290	ATGGCGGATTCGGTGTCTCCGACACCCCGCGCCACCTGGGGCAGAGTGTGACGCTC	349							
Db	241	ATGGCGGATTCGGTGTCTCCGACACCCCGCGCCACCTGGGGCAGAGTGTGACGCTC	300							
QY	350	GTGACCTTCGAGGAGCGTGTGTGAGAGAGGCGCGCTGTGACCGCGCGTGTGGAAG	409							
Db	301	GTGACCTTCGAGGAGCGTGTGTGAGAGAGGCGCGCTGTGACCGCGCGTGTGGAAG	360							
QY	410	TGGGGCTTCCAGCGCGGCTAAAGGAGCAGGAGGCGAGTCCGCCCGGACTGCCAGCGC	469							
Db	361	TGGGGCTTCCAGCGCGGCTAAAGGAGCAGGAGGCGAGTCCGCCCGGACTGCCAGCGC	420							
QY	470	CTGTGGCCCTTGTGAGCTCGCGCTCATGGGCGACACCGCGCTGGCTGGAGGCTCAG	529							
Db	421	CTGTGGCCCTTGTGAGCTCGCGCTCATGGGCGACACCGCGCTGGCTGGAGGCTCAG	480							
QY	530	GGCGGCTG-----GGATGGCTTTTGTACATCTTTCAGGACCCCTTTCACCTGGC	537							
Db	481	GGCGGCTGGGTGAGCAGCGCGGGAACACCGGGAACCGGGCGGGAACCGCGGAAG	540							
QY	538	-----GGATGGCTTTTGTACATCTTTCAGGACCCCTTTCACCTGGC	579							
Db	541	CGCCCCAGGCTGGCAGCGATGGCTTTTGTACATCTTTCAGGACCCCTTTCACCTGGC	600							
QY	580	TTTTTGGAGAAACAGCTGGTCAGGCTTTTCTGTCATGCTTGTAAACAGAGCTTCA	639							
Db	601	TTTTTGGAGAAACAGCTGGTCAGGCTTTTCTGTCATGCTTGTAAACAGAGCTTCA	660							
QY	640	TTATCTCTGACACGATTATTAGTGTTTTAAACCTTTTAAACCGCTTCTACCTGCCAA	699							
Db	661	TTATCTCTGACACGATTATTAGTGTTTTAAACCTTTTAAACCGCTTCTACCTGCCAA	720							
QY	700	CTGTGA 705								
Db	721	CTGTGA 726								

RESULT 7	AC023906	93287 bp	DNA	linear	PRI 06-JUL-2001
LOCUS	Homo sapiens chromosome 15 clone CTD-2184D3 map 15q21.2, complete sequence.				
DEFINITION	AC023906				
ACCESSION	AC023906.7				
VERSION	GI:14595770				
KEYWORDS	HTG				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 93287)				
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T. and Hood, L.				
TITLE	Sequencing of human chromosome 15 D15S146-D15S117 region				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 93287)				
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T. and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-FEB-2000) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA				
REFERENCE	3 (bases 1 to 93287)				
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-JUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
REFERENCE	4 (bases 1 to 93287)				
AUTHORS	Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUL-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA				
COMMENT	On Jul 4, 2001 this sequence version replaced gi:12248292.				
	----- Genome Center				
	Center: Multimegabase Sequencing Center				
	Center code: UWMSC				
	Web site: <a href="http://chroma.mbt.washington.edu/msg_www">http://chroma.mbt.washington.edu/msg_www</a>				
	Contact: <a href="mailto:leerowens@systemsbiology.org">leerowens@systemsbiology.org</a>				
	----- Summary Statistics				
	Sequencing vector: pUC18; L08752				
	Chemistry: Dye-terminator Big Dye; 90% of reads				
	Chemistry: Dye-primer Big Dye; 10% of reads				
	Assembly program: Phrap; version 0.990399				
Note:	Data from overlapping BACs AC010674 [drafting center: UWMSC], AC090970 [drafting center: UWMSC]; and AC016824 [drafting center: GTC] was added for finishing				
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	/note="Data from overlapping clones CTD-250P22 AC090970, RP11-47K1 AC016824, and RP11-430B1 was added and the consensus was determined from CTD-2184D3 to the extent possible"				
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Matches 541; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 64931 GTTGGGGAGCGCACACCATGCGCCAGCCCGCTGCGGGAGCCACCGAGCTGTGCTGGC 64872
Qy 121 CGACTACTGGGTACTGCGCCGGGAACCCGGCACCCCGGAGCCGCCATCCACGCC 180
Db 64871 CGACTACTGGGTACTGCGCCGGGAACCCGGCACCCCGGAGCCGCCATCCACGCC 64812
Qy 181 CGAGGCGCGCTGCTGGGCTCGCGCCGCCAGGTTACCGCAGATTCACCGTCTCTTTT 240
Db 64811 CGAGGCGCGCTGCTGGGCTCGCGCCGCCAGGTTACCGCAGATTCACCGTCTCTTTT 64752
Qy 241 CTCGGCTACTCGGTACTACCCCGGGAAACCGCTTCGAGCTGGTGGCGCTGATCGCGATT 300
Db 64751 CTCGGCTACTCGGTACTACCCCGGGAAACCGCTTCGAGCTGGTGGCGCTGATCGCGATT 64692
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Qy 421 GCCCGCGCTAAAGAGAGAGAGGGCGACGTCGCGCGGACCTGCCAGCGCTGGTGGCTTT 480
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Qy 541 TGGC 544
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ACCESSION AC018903
VERSION AC018903.2 GI:8247797
KEYWORDS HTG; HTG_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  
AUTHORS

TITLE  
JOURNAL

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 214669)  
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,  
Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A.,  
Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.  
Sequencing of human chromosome 15 D15S146-D15S117 region  
Unpublished  
2 (bases 1 to 214669)  
Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,  
Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G.,  
James, R., Kaur, A., Madan, A., Owen, M. P., Ratcliffe, A., Shaffer, T.  
and Hood, L.  
Direct Submission  
Submitted (22-DEC-1999) Multimegabase Sequencing Center, University  
of Washington, PO BOX 357730, Seattle, WA 98195, USA  
On Jun 4, 2000 this sequence version replaced gi:6630517.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UMWSC  
Web site: http://chroma.mbt.washington.edu/msg\_www  
Contact: leerowens@systemsbiology.org  
----- Summary Statistics  
Sequencing vector: pUC18; 108752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
-----  
\* NOTE: This record contains 192 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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907: contig of 1162 bp in length  
2068: gap of unknown length  
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4385: contig of 817 bp in length  
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Matches 348; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 656 TTATTATGAGTTTTAAACCTTTTAAACCCGCTTCTACCTGCCCACTGTGACCACTAAAT 715
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Qy 716 GACAGATGCTGTGAGAACAGAACTGAGGGAACACCTTCCCTCCACCCAGAGCTTTTAA 775
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RESULT 9
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VERSION AC018903.2 GI:8247797
KEYWORDS HTG; HTGS PHASE0.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
Madan,A., Nesbitt,R., Shaffer,T. and Hood,L.
Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
2 (bases 1 to 214669)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
and Hood,L.
Direct Submission
Submitted (22-DEC-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Jun 4, 2000 this sequence version replaced gi:6630517.
----- Genome Center
Center: Multimegabase Sequencing Center
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; 108752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
-----
* NOTE: This record contains 192 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 10906 11006: contig of 1147 bp in length
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18578: contig of 854 bp in length
18678: gap of unknown length
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51433: gap of unknown length
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J. Biol. Chem.	273 (49),	32479-32486	(1998)
JOURNAL	9047817		
MEDLINE	PUBMED		
REFERENCE	2 (bases 1 to 1225)		
AUTHORS	Irohara,N. and Nunez,G.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAY-1998)		
	Department of Pathology, University of Michigan Medical School, 1500 E.Medical Dr., Ann Arbor, MI 48109, USA		
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QY	146	GAACCCGGCACCCCGAGCGCGGCATCCAGCCGAGCGCGCGTGTGCGCTCCCGG	205
Db	218	GAGCCGACACCCCGAGCGCACCGCCACGTGTGTGAGCGCGCTTGTCTCGCTCTGTG	277
QY	206	GCCGCCAGGTATGGCAGATTACCGGTCCTTTTCTCCGCCCTACCTCGGTACCCCGGG	265
Db	278	ACTAGGCAGATCCAGCAGGAGCACCAAGAAATTTTTTCTCTCTCTCGAAAGCGGGGC	337
QY	266	AACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCGTCGCTCTCCGACAGCCCGGCC	325
Db	338	AATCGCTCGAGCTGGTGAACAGATGGCAGATAGTTGCTCTCCAGACCAAGACTTC	397
QY	326	ACCTGGGGCAGTGGTGACGCTCTGACCTTCGAGGACGCTGCTGAGAGAGGGCGG	385
Db	398	AGCTGGAGCCAACTGGTGATGCTCTCTGGCCTTCGCGGGACGCTTATGAATCAAGGCC	457
QY	386	CTGCTGACCGCCCGGTGGAGAGTGGGGCTCCAGCCCGGCTAAAGAGCAGAGAGGC	445
Db	458	TACATGGCTGTCAAGCAGAAGA-----GGGATCTGGGGAAATCGTGTC	499
QY	446	GACGTCGCCGGGACTGCCAGCCCTGGTGGCTTGTCTGAGCTCGCGGCTAATGGG---	502
Db	500	ATAGTGACCCGAGACTGCTCTCTAGTGAATTTCTGTATAATCTGCTCATGGGGGCT	559
QY	503	CAGCAGCGCGCTGGCTGACGGCTCAGGCGGCTGGGATGGCTTTTGTCACTTCTTCAG	562
Db	560	CGGACCGCGCCAGCTGGAGGCTCTCGCGGCTGGATGGCTTTTTCGCTTCTTCAAG	619
QY	563	ACCCCTTTCACCTGGCTTTTTCGAGAAACAGCTGGTCCAGGCTTTCTGTCACTGCTG	622
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QY 683 CGGTTTACTGCGCACTGTGACCAACTAAATGACAGATGTGTGAGAACAGAACTGAG 742
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Db 855 TTGTGATGGCCAGCATTTGAAGGGGCCCATGTA 890

RESULT 12
BC052690
LOCUS
DEFINITION
Mus musculus Bcl2-like 10, mRNA (cDNA clone MGC:60542
IMAGE:30052580), complete cds.
ACCESSION
BC052690
VERSION
MGC.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1257)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stachenko,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carrincci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Rulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahney,J., Hellon,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
2 (bases 1 to 1257)
Strausberg,R.
Direct Submission
Submitted (16-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Minoru Ko
cDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: http://igsun.grc.nia.nih.gov/cDNA/)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov

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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Tsurgenc, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov> Series: IRAK Plate: 112 Row: h Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7304926.

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Best Local Similarity 63.0%; Pred. No. 6.9e-35;
Matches 476; Conservative 0; Mismatches 254; Indels 26; Gaps 4;

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Db 220 GAGCCGACACCCCGAGCGCGGCATCTGTCTGAGCGCGCTTGTCTGCTGCTGTG 279
QY 206 GCGCCAGGTTACGGCAGATTCACCGTCTCTTTCTCGCCCTACCTCGGCTACCCCGG 265
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Db 340 AATCGCTGGAGCTGTGTAACAGATGGCAGATAAGTGTCTCTCAAGACCAAGACTTC 399
QY 326 ACTGGGGGAGCTGTGACGCTCGTCACTTCGAGGAGCGCTGCTGGAGAGGGCGG 385
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RESULT 13  
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LOCUS  
DEFINITION Rattus norvegicus BCL2L10 (Bcl2l10) mRNA, complete cds.

ACCESSION AY029163  
VERSION AY029163.1 GI:13641257  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 1074)  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Bcl-2-related protein family gene expression during oligodendroglial differentiation  
J. Neurochem. 85 (6), 1500-1512 (2003)  
MEDLINE 22672518  
PUBMED 12787069  
REFERENCE 2 (bases 1 to 1074)  
AUTHORS Itoh,T., Itoh,A. and Pleasure,D.  
TITLE Direct Submission  
JOURNAL Submitted (29-MAR-2001) Neurology Research, The Children's Hospital of Philadelphia, Abramson Research Center, Room 516 I, 3517 Civic Center Boulevard, Philadelphia, PA 19104, USA

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## ORIGIN

Query Match 27.5%; Score 244.2; DB 10; Length 1074;  
Best Local Similarity 61.7%; Pred. No. 1.5e-32;  
Matches 455; Conservative 0; Mismatches 253; Indels 29; Gaps 3;  
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QY 140 GCCCGGAACCCCGCACCCCGGAGCGGCCCATCCAGCCCGGAGCGCGCTGCTGCGC 199  
Db 72 GCACGGCGCGGAACACCCCTGAGCCACCTGAGCCACCTGTTGAGGCGGCTTGTGCGC 131  
QY 200 TCCGCGCGCGCAGGTTACGGCAGATTCACCGGTCTCTTTCTCCGCTACCTCGGCTAC 259  
Db 132 TCTGTGACTAGTCAGATCCCAACAGGAGCACAGATCTTTTCACTCTTCCGCGACTAC 191  
QY 260 CCCGGGAACCCGCTTCGAGCTGCTGGCGCTGATGGCGGATTCGCTCTCCGACAGCCCC 319  
Db 192 CAGGCGAACCCCTGAGCTGGTGCACAGATGGCGATGAGTTGCTTCCAATGACCAA 251  
QY 320 GGGCCCACTTGGGCGCAGATGCTGACCTGACCTTCCAGGAGCGCTGCTGGAGAGA 379  
Db 252 GAGTTCAACTGGGCGCGCTGCTGCTGCGCTTCTGGGAGCGCTAATGAACCAA 311  
QY 380 GGGCGCTGCTGACCGCGCGCTGGAAGAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAG 439  
Db 312 GACGAGCTGTTAAGCGGAGGAGGATCAAGAAACCGTCTCTCTAC----- 357  
QY 440 GAGGCGCAGCTGCGCGCGGAGCTGCGAGCGCTGGTGGCTTGTGAGCTCGCGCTCATG 499  
Db 358 -----TGGAGCGAGACTGCTATCTCATAGTGAAGTTGCTGACAACTGACACCA 407  
QY 500 GGGCAGCAGCGCGCTGCTGCGGCTCAGGCGCTCAGGCGCTGGGATGGCTTTTGTCTCTTC 559  
Db 408 GGACGGCATGCTCTCGGCTGGAGGCTCAGGCTGGGATGGCTTTTGGCAATCTTC 467  
QY 560 AGGACCCCTTTCACCTGGCTTTTGGAGAAACAGCTGCTCAGGCTTTTCTGCTATGC 619  
Db 468 AAGAACCCCTTACCAACCGCGCTTCTGGAGAAAGTTGCTGATCCGGGCTATTCTGCTGT 527  
QY 620 TTGTTAAACAGCGCTTCATTTATCTCTGACAGCATTTATATGAGTTTAAACTTTTA 679  
Db 528 TTTCTTGAACGGCCATCTTTTATATCTGGAATGTTTAT-----AGTTTTAAATTTT 583  
QY 680 ACCCGCTTCTACCTGCGCAACTGTGACCAACTAAATGACAGATGTGTGAGAACAGAACT 739  
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QY 740 GAGGGAAGACCTTCCCGCAGCGCTTTTATCTGAATGCATACAGGAGCTCTG 799  
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Db 703 GGTGGGATGGGCTA 719

RESULT 14  
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LOCUS  
DEFINITION Mus musculus chromosome 9 clone RP24-18912, WORKING DRAFT SEQUENCE,  
3 unordered pieces.

ACCESSION AC133947  
VERSION AC133947.2 GI:50199129  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

AC133947 169914 bp DNA linear HTG 10-JUL-2004

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 169914)  
Wilson.R.K.  
The sequence of Mus musculus clone  
Unpublished  
2 (bases 1 to 169914)  
McPherson,J.D. and Waterston,R.H.  
Direct Submission  
Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 169914)  
Wilson.R.K.  
Direct Submission  
Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
On Jul 10, 2004 this sequence version replaced gi:23238076.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@wustl.wustl.edu  
----- Project information -----  
Center project name: M\_BB0189102  
----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 167792 bases at least Q40  
Consensus quality: 168148 bases at least Q30  
Consensus quality: 168291 bases at least Q20

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 21204: contig of 21204 bp in length  
\* 21205 21304: gap of unknown length  
\* 21305 86045: contig of 64741 bp in length  
\* 86046 86145: gap of unknown length  
\* 86146 169914: contig of 83769 bp in length.

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83535 GAGCCGACACCCCGAGAGCCACCGCCACCTGTGTCGAGCGCGCTTGTCTGCTGTG 83594  
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QY 206 GCGCCAGGTTAGGCGAGATTCAAGGCTCTTTTCTCGGCTACCTCGGCTACCCGGG 265  
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DB 83877 CGGACCGCGCGAGGCTGGAGGCTCTCGGCGGTGG 83913  
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## RESULT 15

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Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., DeAtellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gram, L., Grand-Pierre, N., Hafez, N., Hagoopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, C., Rogov, P., Retchuk, A., Ramaeamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

Submitted (28-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 202851)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., DeAtellano, K., Diaz, J.S., Ferreira, P., Fitzgerald, M., Gage, D., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Hafez, N., Galagan, J., Gardyna, S., Gram, L., Grand-Pierre, N., Hafez, N., Hagoopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Retta, R., Rise, C., Rogov, P., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Seaman, S., Severy, P., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## COMMENT

Submitted (02-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 2, 2004 this sequence version replaced gi:44681569.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: [sequence\\_submissions@broad.mit.edu](mailto:sequence_submissions@broad.mit.edu)

Project Information

Center project name: L24773

Center clone name: 365\_N15

Location/Qualifiers

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repeat_region 15724..15775

Query Match 16.6%; Score 147; DB 10; Length 202851;
Best Local Similarity 61.5%; Pred. No. 6.9e-16;
Matches 281; Conservative 0; Mismatches 155; Indels 21; Gaps 2;

QY 86 GACCCGCTCGGAGCGACCGAGCTGTGCTGGCGGACTACTGGGTACTGGCGCCCGG 145
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 146 GAACCGGACCCCGGAGCGCGGCATCCAGCCCGAGCGCGCGTGTGGCTTCCGCG 205
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 206 GCGCGAGGTACGGCAGATTACCGGTCTTTTCTCGCCCTACTCGGCTACCCCGG 265
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30472 ACTAGGCAGATCCAGCAGGAGCACCAGAAATTTTCTCTCTGCGAAAGCGGGGC 30531
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 AACCGCTTCGAGCTGTGGCGGTGATGGCGGATTCGGTCTCTCGGACAGCCCGCCCGCC 325
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30532 AATCGCTGGAGCTGTGTAACAGATGGCAGATAAGTTGCTCTCCAAGACCAAGACTTC 30591
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 326 ACCTGGGGCAGAGTGTGACGCTCGTGACCTTCGAGGAGCGCTGCTGGAGAGGGCGG 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30592 AGCTGAGGCAACTGGTGTATGCTCTGCGCTTCGCGGGAGCGCTTATGAATCAGGCCCT 30651
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 386 CTGGTGACCGCGCGGTGGAGAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAGGAGGC 445
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30652 TACATGGCTGTCAAGCAGAAGA-----GGGATCTGGGGAATCGTGTG 30693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 445 GACGTGCGCCCGGACTGCGAGCGCTGTGGCGCTTGTGAGCTCGCGGCTATGGG--- 502
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30694 ATAGTGACCCGAGACTGTGTCTCATAGTGAATTTCTGTATAATCTGTCATGGGGGT 30753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 503 CAGCACCGGCGCTGGCTGAGGCTCAGGCGGCTGGG 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 30754 CGCACCGCGCAGGCTGAGGCTCTCGCGGCTGGG 30790
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: November 7, 2004, 01:20:03  
Job time : 6240 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 7, 2004, 03:03:17 ; Search time 510 Seconds

(without alignments)  
2099.768 Million cell updates/sec

Title: US-10-071-174-2

Perfect score: 1084  
Sequence: 1 MVDQRLRTTMDPLRERTE.....QAFUSCLLTAFIVLWTRLL 204

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-MODE=LOCAL -CUFFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

- Database :
- N\_Geneseq\_23Sep04:\*
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  - 5: Geneseqn2001bs:\*
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  - 7: Geneseqn2002bs:\*
  - 8: Geneseqn2003as:\*
  - 9: Geneseqn2003bs:\*
  - 10: Geneseqn2003cs:\*
  - 11: Geneseqn2003ds:\*
  - 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1084	100.0	887	AAD46683	Human Bcl
2	1045	96.4	1168	Aaz90049	Hydrophob
3	1035	95.5	582	Aaz90039	Hydrophob
4	701	64.7	522	Aah47022	Human Bcl
5	639	58.9	548	Abk41913	cdNA enco
6	639	58.9	548	ADB59580	Connectiv

7	559	51.6	874	6	ABQ44403	Abq44403 Oligonuc
c	559	51.6	874	6	ABQ44402	Abq44402 Oligonuc
9	513	47.3	874	6	ABQ44404	Abq44404 Oligonuc
c	513	47.3	874	6	ABQ44405	Abq44405 Oligonuc
11	475.5	43.9	650	10	ADD34132	Add34132 Mouse mit
c	232.5	21.4	835	10	ADD34582	Add34582 Mouse mit
13	199	18.4	338	10	ADD34583	Add34583 Mouse mit
14	129	11.9	658	6	ABT09344	Abt09344 Phase-1 R
15	129	11.9	658	10	ADG30848	Adg30848 Liver tox
16	129	11.9	658	12	ADG45405	Adg45405 Liver inf
17	129	11.9	658	12	ADH222707	Adh222707 Partial D
18	127	11.7	579	10	ADH26628	Adh26628 Human Bax
19	127	11.7	579	2	AAZ19764	Aaz19764 Human wil
20	127	11.7	579	4	AAC84598	Aac84598 Human Bax
21	127	11.7	579	6	AAC90811	Aac90811 Human Bax
22	127	11.7	579	6	ABV78149	Abv78149 Human Bax
23	127	11.7	579	6	ABZ35725	Abz35725 Human Bax
24	127	11.7	579	6	ABX09968	Abx09968 Human Bax
25	127	11.7	579	6	ABL91690	AbL91690 Human pol
26	127	11.7	579	9	ADA20845	Ada20845 Human BAX
27	127	11.7	579	9	AAL61054	Aal61054 Human BAX
28	127	11.7	579	11	ADI32061	Adi32061 Human cDN
29	127	11.7	579	12	ADO05979	Ado05979 Pro-apopt
30	127	11.7	624	2	AAQ97606	Aaq97606 Human Bax
31	127	11.7	779	2	AAZ15935	Aaz15935 Human gen
32	127	11.7	791	2	AAZ77545	Aaz77545 Human ova
33	127	11.7	996	2	AAZ06732	Aaz06732 Nucleotid
34	126	11.6	677	9	ADA20844	Ada20844 Human BAX
35	125	11.5	624	2	AAV84005	Aav84005 cDNA enco
36	125	11.5	624	4	AAF77704	Aaf77704 Human bcl
37	120	11.1	596	2	ADF39373	Adf39373 Human BAX
38	120	11.1	1607	2	ADF39391	Adf39391 Human BAX
39	119	11.0	579	10	ADB52764	Adb52764 Primary r
40	119	11.0	579	10	ABT41943	Abt41943 Toxicity
41	118	10.9	579	6	AAF88666	Aaf88666 C. albica
42	118	10.9	583	2	AAT96577	Aat96577 Human bcl
43	118	10.9	583	2	AAZ25134	Aaz25134 Human bcl
44	117.5	10.8	581	2	AAT96578	Aat96578 Mouse bcl
45	117.5	10.8	581	2	AAZ25135	Aaz25135 Mouse bcl

ALIGNMENTS

RESULT 1  
AAD46683  
ID AAD46683 standard; DNA; 887 BP.  
XX  
AC AAD46683;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Human Bcl-B DNA.  
XX  
KW Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder;  
KW proliferative disorder; muscle degeneration; Alzheimer's disease; CJD;  
KW Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic;  
KW Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia;  
KW SCA; dentatorubropallidoluysian atrophy; DRPLA; Kennedy's disease;  
KW stroke; ischaemia; head trauma; neuroprotection; anticonvulsant; vulnery;  
KW neurotropic; neuroprotective; cyostatic; immunosuppressive; vasotropic;  
KW cerebroprotective; autoimmune disorder; chromosome 15; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 50..664  
FT /tag= a  
FT /product= "Human Bcl-B protein"

PF	07-FEB-2002; 2002WO-US003547.	Db	470	CTGGTGGCCCTGCTGAGCTCGGCGCTCATGGGCGACACCGCGCTGGCTGCAGGCTCAG	529
XX					
PR	07-FEB-2001; 2001US-0267166P.	Qy	161	GlyGlyTyrAspGlyPheCysHisPhePheArgThrProPheProLeuAlaPheTrpArg	180
PR	07-FEB-2002; 2002US-00071174.				
XX		Db	530	GGCGGCTGGGATGGCTTTTGTCACCTTCTTCAGACCCCTTTCCACTGGCTTTTGGAGA	589
XX	(BURN-) BURNHAM INST.				
XX		Qy	181	LysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrAlaPheLeuTyrLeuTrp	200
PI	Reed JC, Ke N, Godzik A;				
XX	WPI; 2002-723312/78.	Db	590	AAACAGCTGGTCAGGCTTTTCTGTCATGCTTGTAAACACAGCCTTCATTATCTCTGG	649
DR	P-PSDB; AAE29097.				
XX		Qy	201	ThrArgLeuLeu 204	
XX		Db	650	ACACGATTATTA 661	
PT	New isolated or recombinant Bcl-B nucleic acids and polypeptides, for				
PT	treating a disorder associated with apoptosis, such as cell degenerative				
PT	or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's				
PT	disease.				
XX	Claim 11; Page 74; 82pp; English.				
XX					
CC	The invention relates to human member of Bcl-2 family Bcl-B protein and				
CC	its corresponding nucleic acid. Bcl-B is useful in treating a subject				
CC	having or at risk of a disorder associated with apoptosis, such as cell				
CC	degenerative or proliferative disorder like neural or muscle				
CC	degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease				
CC	(CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's				
CC	disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6),				
CC	dentatorubropallidolysian atrophy (DRPLA), Kennedy's disease, stroke,				
CC	ischemia, head trauma, neoplasia, autoimmune disorder or fibrotic				
CC	condition. The transgenic animals are used as in vivo models to study				
CC	apoptosis and potential therapies for apoptosis. The present sequence is				
CC	human Bcl-B DNA. Bcl-B gene is located at chromosome 15				
XX					
SQ	Sequence 887 BP; 171 A; 270 C; 269 G; 177 T; 0 U; 0 Other;				
Alignment Scores:					
Pred. No.:	1.16e-96	Length:	887		
Score:	1084.00	Matches:	204		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-10-071-174-2 (1-204) x AAD46683 (1-887)					
Qy	1 MetValAspGlnLeuArgGluArgThrThrMetAlaAspProLeuArgGluArgThrGlu 20				
Db	50 ATGGTTGACAGTTCGGGAGCGCACCATGGCGGCCCGCTGGCGGAGCGCACCGAG 109				
Qy	21 LeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40				
Db	110 CTGTTGCTGGCCGACTACCTCGGGGTACTGCGCCGGGACCCCGGACCCCGGAGCGGG 169				
Qy	41 ProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnLeuHis 60				
Db	170 CCATCCAGCCCGGAGCGCGCGTCTCGCTCCGCGCGCCAGTACCGCAGATTAC 229				
Qy	61 ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu 80				
Db	230 CGGTTCCTTTTCCCGCTACCTCGGCTACCCCGGGAACCGCTTCGAGCTGGTGGCGCTG 289				
Qy	81 MetAlaAspSerValLeuSerAspSerProGlyProThrTrpGlyArgValValThrLeu 100				
Db	290 ATGGCGATTCCGTTGCTCTCGACAGCCCGCGCCACCTGGCGGAGTGGTGGAGCTC 349				
Qy	101 ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTrpLysLys 120				
Db	350 GTGACCTTCGCGGAGCGCTGCTGGAGAGAGGCGCGCTGTGACCCCGCGTGGAGAGAG 409				
Qy	121 TrpGlyPheGlnProArgLeuLysGluGlnGluGlyAspValAlaAlaArgAspCysGlnArg 140				
Db	410 TGGGGCTTCAGCCCGCGCTTAAGGACGAGAGGGGCGACGCTCCCGCGGACTGCCAGCGC 469				
Qy	141 LeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGln 160				

161 GlyGlyTyrAspGlyPheCysHisPhePheArgThrProPheProLeuAlaPheTrpArg 180

530 GGCGGCTGGGATGGCTTTTGTCACCTTCTTCAGACCCCTTTCCACTGGCTTTTGGAGA 589

181 LysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrAlaPheLeuTyrLeuTrp 200

590 AAACAGCTGGTCAGGCTTTTCTGTCATGCTTGTAAACACAGCCTTCATTATCTCTGG 649

201 ThrArgLeuLeu 204

650 ACACGATTATTA 661

RESULT 2

AAZ90049 ID AAZ90049 standard; cDNA; 1168 BP.

XX AC AAZ90049;

XX 09-MAY-2000 (first entry)

XX Hydrophobic domain containing protein clone HP02403 nucleotide sequence.

XX Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV;

XX cell proliferation; immune stimulant; immune deficiency; tumour; pain;

XX rheumatoid arthritis; insulin dependent diabetes mellitus; fertility;

XX myasthenia gravis; haematopoiesis regulator; tissue growth; depression;

XX anti-inflammatory; infection; bodily characteristic; ss.

XX Homo sapiens.

XX WO200000506-A2.

XX 06-JAN-2000.

XX 18-JUN-1999; 99WO-JP003242.

XX 26-JUN-1998; 98JP-00180008.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI; 2000-160665/14.

XX P-PSDB; AAY78802.

XX Novel human proteins having hydrophobic domains used for research and diagnostic purposes.

XX Claim 4; Page 92-94; 117pp; English.

XX This sequence represents the hydrophobic domain containing protein, clone HP00631 nucleotide sequence. The sequence is isolated from a human stomach cancer cell line. The HP02403 protein contains one putative transmembrane domain. The protein shows homology to the Japanese quail apoptosis regulator NR-13. The invention relates to human proteins with hydrophobic domains, the DNA and the cDNA encoding them. The polynucleotides and proteins are predicted to have biological activities which make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity (nutritional source or supplement); cytokine and cell proliferation/differentiation activity; immune stimulating (e.g. as vaccines) or suppressing activity (e.g. to treat various immune deficiencies such as SCIDS or HIV, connective tissue disease, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease, as well as asthma, allergies and organ transplantation); haematopoiesis regulating activity (e.g. in treatment of myeloid or lymphoid cell deficiencies); tissue growth

CC activity (e.g. wound healing and tissue repair, ulcers, burns,  
CC periodontal disease); activin/inhibin activity; chemotactic/chemokinetic  
CC activity; haemostatic and thrombolytic activity (e.g. treating  
CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and  
CC tumour inhibition activity. The polynucleotides are also stated to be  
CC useful for gene therapy. Other activities include inhibiting infections  
CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis,  
CC malaria); effecting bodily characteristics such as, e.g. weight, colour,  
CC skin, effecting biorhythms or cardiac cycles; enhancing fertility;  
CC treatment of depression; treatment of pain; hormonal or endocrine  
CC activity. The polynucleotides may also be used for recombinant expression  
CC of the protein  
XX

SQ Sequence 1168 BP; 276 A; 312 C; 300 G; 280 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,09e-92 Length: 1168  
Score: 1045.00 Matches: 136  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 96.40% Indels: 0  
DB: 3 Gaps: 0

US-10-071-174-2 (1-204) x AA290049 (1-1168)

QY 9 ThrThrMetAlaAspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeuGly 28  
Db 1 ACCACCATGGCCGACCGCTGGGGAGCGACCGAGCTGTTCGCGCGACTACCTGGGG 60  
QY 29 TyrCysAlaArgGluProGlyThrProGluProAlaProSerThrProGluAlaVal 48  
Db 61 TACTGCGCGGGAAACCGCGACCCCGAGCGCGGCCATCCACGCCGAGGCCCGCGTG 120  
QY 49 LeuArgSerAlaAlaAlaArgLeuArgGlnIleHisArgSerPhePheSerAlaTyrLeu 68  
Db 121 CTGCGCTCCGCGCGCGCCAGGTACGCGAGATTCACCGGTCTCTTTCTCCGCTACCTC 180  
QY 69 GlyTyrProGlyValAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAsp 88  
Db 181 GGCTACCCCGGAGACCGCTTCAGCTGTGGCGCTGATGGCGGATTCGCTCTCCGAC 240  
QY 89 SerProGlyProThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeu 108  
Db 241 AGCCCGCGGCCACCTGGGGCAGAGTGTGACGCTCGTGACCTTCGACGGAGCGCTGTG 300  
QY 109 GluArgGlyProLeuValThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLys 128  
Db 301 GAGAGAGGGCCGCTGTGTACCCCGCGGTGGAAGAAGTGGGGCTTCACGCCGCGGCTAAAG 360  
QY 129 GluGlnGluGlyAspValAlaAlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArg 148  
Db 361 GAGCAGAGGGCGCGCTGCGCCGCGGACTGCCAGCGCTGTGGCTTGTGAGCTCGCGG 420  
QY 149 LeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyTrpAspGlyPheCysHis 168  
Db 421 CTCATGGGGCAGCAGCCGCGCTGGCTGCAGGCTCAGGGCGGCTGGGATGGCTTTGTGCAC 480  
QY 169 PhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeu 188  
Db 481 TTCTTCAGACCCCTTCCATCGCTTTTGGAGAAACAGCTGGTCAGGCTTTTCTG 540  
QY 189 SerCysLeuLeuThrThralaPheLeuTyrLeuTrpThrArgLeuLeu 204  
Db 541 TCATGCTTGTAAACACAGCGCTTCATTTATCTCTGACACGATTATTA 588

RESULT 3

AA290039

ID AA290039 standard; cDNA; 582 BP.

XX

AC AA290039;

XX

DT 09-MAY-2000 (first entry)

XX

DE Hydrophobic domain containing protein clone HP02403 coding sequence.  
XX  
KW Hydrophobic domain; clone HP02403; nutritional supplement; SCID; HIV;  
KW cell proliferation; immune stimulant; immune deficiency; tumour; pain;  
KW rheumatoid arthritis; insulin dependent diabetes mellitus; fertility;  
KW myasthenia gravis; haematopoiesis regulator; tissue growth; depression;  
KW anti-inflammatory; infection; bodily characteristic; ss.  
OS Homo sapiens.  
XX  
PN WO200000506-A2.  
XX  
PD 06-JAN-2000.  
XX  
PF 18-JUN-1999; 99WO-JP003242.  
PR 26-JUN-1998; 98JP-00180008.  
XX  
PA (SAGA) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
XX  
PI Kato S, Kimura T;  
XX  
DR WPI; 2000-160665/14.  
DR P-PSDB; AAY78802.  
XX  
PT Novel human proteins having hydrophobic domains used for research and  
PT diagnostic purposes.  
XX  
PS Claim 3; Page 84; 117pp; English.  
XX  
CC This sequence represents the hydrophobic domain containing protein, clone  
CC HP00631 coding region. The sequence is isolated from a human stomach  
CC cancer cell line. The HP02403 protein contains one putative transmembrane  
CC domain. The protein shows homology to the Japanese quail apoptosis  
CC regulator NR-13. The invention relates to human proteins with hydrophobic  
CC domains, the DNA and the cDNA encoding them. The polynucleotides and  
CC proteins are predicted to have biological activities which make them  
CC suitable for treating, preventing or ameliorating medical conditions in  
CC humans and animals. Suggested activities include nutritional activity  
CC (nutritional source or supplement); cytokine and cell  
CC proliferation/differentiation activity; immune stimulating (e.g. as  
CC vaccines) or suppressing activity (e.g. to treat various immune  
CC deficiencies such as SCIDS or HIV, connective tissue disease, systemic  
CC lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary  
CC inflammation, Guillain-Barre syndrome, myasthenia gravis, graft-versus-host disease  
CC and autoimmune inflammatory eye disease, as well as asthma, allergies and  
CC organ transplantation); haematopoiesis regulating activity (e.g. in  
CC treatment of myeloid or lymphoid cell deficiencies); tissue growth  
CC activity (e.g. wound healing and tissue repair, ulcers, burns,  
CC periodontal disease); activin/inhibin activity; chemotactic/chemokinetic  
CC activity; haemostatic and thrombolytic activity (e.g. treating  
CC haemophilias); receptor/ligand activity; anti-inflammatory activity; and  
CC tumour inhibition activity. The polynucleotides are also stated to be  
CC useful for gene therapy. Other activities include inhibiting infections  
CC caused by bacteria, fungi, viruses and other parasites (e.g. Hepatitis,  
CC malaria); effecting bodily characteristics such as, e.g. weight, colour,  
CC skin, effecting biorhythms or cardiac cycles; enhancing fertility;  
CC treatment of depression; treatment of pain; hormonal or endocrine  
CC activity. The polynucleotides may also be used for recombinant expression  
CC of the protein  
XX  
SQ Sequence 582 BP; 85 A; 193 C; 191 G; 113 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.28e-92 Length: 582  
Score: 1035.00 Matches: 194  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 95.48% Indels: 0  
DB: 3 Gaps: 0

US-10-071-174-2 (1-204) x AA920039 (1-582)

QY 11 MetAlaAspProLeuArgGluArgThrGluLeuLeuLeuAlaAspTyrLeuGlyTyrCys 30  
Db 1 ATGGCCGACCGCTGGGAGCGCACCAGCTGTTCCTGGCCGACTACCTGGGTACTGC 60  
QY 31 AlaArgGluProGlyThrProGluProAlaProSerThrProGluAlaAlaValLeuArg 50  
Db 61 GCCCGGGAACCGCGACCCCGCGCGCGCCATTCACGCCCGCGCGCGCTGTGGCG 120  
QY 51 SerAlaAlaAlaArgLeuArgGlnIleHisArgSerPheSerAlaTyrLeuGlyTyr 70  
Db 121 TCCGCGCGCCGAGGTTCAGCGAGATTACCGGTCTCTTTCTCGCGCTACCTCGCTAC 180  
QY 71 ProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerPro 90  
Db 181 CCCGGGAACCGCTTCAGCTGGTGGCGCTGATGGCGATTCCGTCTCCGACAGCCCC 240  
QY 91 GlyProThrTyrGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArg 110  
Db 241 GCGCCACCTGGGCGAGAGTGTGACGCTCGTACCTTCGACGGAGCGCTGTGGAGAGA 300  
QY 111 GlyProLeuValThrAlaArgTyrLysLysTyrGlyPheGlnProArgLeuLysGluGln 130  
Db 301 GGGCCGCTGTGACCGCCCGGTGGAAAGTGGGGCTTCACGCCCGCGCTAAAGGAGCAG 360  
QY 131 GluGlyAspValAlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArgLeuMet 150  
Db 361 GAGGGGACGTCGCCGGGACTCCGACGCGCTGTGGCTTGTGAGCTCGCGGCTCATG 420  
QY 151 GlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyTyrTrpAspGlyPheCysHisPhe 170  
Db 421 GGGCAGCACCGCGCTGGCTGCGAGGTCAGGGCGGCTGGGCTTTGTCACTTCTTC 480  
QY 171 ArgThrProPheProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCys 190  
Db 481 AGACCCCGCTTCCACGCGCTTTTGGAGAAACAGCTGTGTCAGGCTTTTCTGTATGC 540  
QY 191 LeuLeuThrThrAlaPheLeuTyrLeuTyrTrpArgLeuLeu 204  
Db 541 TTGTATACACAGCTTCACTTATCTCTGGACACGATTATTA 582

RESULT 4  
AAH47022 ID AAH47022 standard; cDNA; 522 BP.

AC AAH47022;  
XX 29-OCT-2001 (first entry)  
XX Human Bcl-2-like polypeptide encoding cDNA (clone HLIB840).  
XX Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;  
XX respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;  
XX immunosuppressive; antiinflammatory; gene therapy; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 44..448  
XX /\*tag= a  
XX /product= "Bcl-2-like polypeptide"  
XX /note= "gene No. 2"  
XX WO200157060-A1.  
XX 09-AUG-2001.  
XX 31-JAN-2001; 2001WO-US003080.  
XX 01-FEB-2000; 2000US-0179487P.  
XX 07-FEB-2000; 2000US-0180697P.  
XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Duan DR, Ni J;  
XX WPI; 2001-476279/51.  
XX P-PSDB; AAB85666.  
XX Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
XX preventing, diagnosing and/or treating.  
XX Claim 1; Page 276; 285pp; English.

XX The invention provides nucleic acid molecules (NAMI) encoding 4 human Bcl  
XX -2-like polypeptides (PEPI). The NAMI and PEPI may be used in the  
XX prevention, diagnosis and treatment of diseases associated with  
XX inappropriate Bcl-2-like polypeptides' expression. The NAMI may be used  
XX to produce the soluble Bcl-2-like polypeptides by standard recombinant  
XX methodology. The polypeptides may also be used as antigens in the  
XX production of antibodies against Bcl-2 and in assays to identify  
XX modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
XX and antagonists may be used to down regulate expression and activity. The  
XX anti-PEPI antibodies may also be used as diagnostic agents for detecting  
XX the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
XX immunosorbant assay (ELISA)). Disorders that may be prevented, diagnosed  
XX and/or treated by the above methods include, immunodeficiencies (e.g. a  
XX gammaglobulinemia and B cell lymphoproliferative disorder), allergic  
XX disorders (e.g. rheumatoid arthritis and Grave's disease), allergic  
XX reactions, inflammations, respiratory diseases and cardiovascular  
XX disorders (a full list of disorders is given in the specification). The  
XX present sequence represents a human Bcl-2-like polypeptide encoding cDNA  
XX Sequence 522 BP; 102 A; 148 C; 154 G; 118 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.96e-59 Length: 522  
Score: 701.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.67% Indels: 0  
Gaps: 4

US-10-071-174-2 (1-204) x AAH47022 (1-522)

QY 75 PheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerProGlyProThrTyr 94  
Db 3 TTCGAGCTGGTGGCGCTGATGGGGATTCCGTGCTCTCCGACAGCCCGCGCCACCTGG 62  
QY 95 GlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuVal 114  
Db 63 GGCAGAGTGGTGGCGCTGTCGACCTTCGAGGGGAGCTGCTGGAGAGGGCGGCTGGTG 122  
QY 115 ThrAlaArgTyrLysLysTyrGlyPheGlnProArgLeuLysGluGlnGlyAspVal 134  
Db 123 ACCGCCCGCTGGAGAGTGGGGCTTCACGCCCGGCTAAAGAGAGGAGGGCGAGCTC 182  
QY 135 AlaArgAspCysGlnArgLeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArg 154  
Db 183 GCCCGGAGCTGCCAGCGCTGGTGGCTTGTGAGCTCGCGGCTCATGGGGCAGCACCGC 242  
QY 155 AlaTrpLeuGlnAlaGlnGlyTyrAspGlyPheCysHisPhePheArgThrProPhe 174  
Db 243 GCTTGGCTGCGAGGCTCAGGGCGGCTGGAGTGGCTTTTGTACATCTTTCAGGACCCCTTT 302  
QY 175 ProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrThr 194  
Db 303 CCACCTGGCTTTTGGAGAAAACAGCTGCTCCAGGCTTTTCTGTCTATGCTTTTAAACACA 362  
QY 195 AlaPheLeuTyrLeuTyrThrArgLeuLeu 204  
Db 363 GCTTTCATTTATCTCTGGACACGATTATTA 392  
RESULT 5  
ABK41913

ID ABK41913 standard; cDNA; 548 BP.  
XX  
AC ABK41913;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE cDNA encoding novel human connective tissue related polypeptide #301.  
XX  
KW Human; connective tissue related disorder; cancer; gene therapy;  
KW cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO20015343-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001322.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
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PR 18-APR-2000; 2000US-0198123P.  
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PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
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PR 14-AUG-2000; 2000US-0224518P.  
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PR 17-NOV-2000; 2000US-0249265P.  
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PR 17-NOV-2000; 2000US-0249299P.  
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08-DEC-2000; 2000US-0251989P.  
08-DEC-2000; 2000US-0251990P.  
11-DEC-2000; 2000US-0254097P.  
05-JAN-2001; 2001US-0259678P.  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-565190/63.  
P-PSDB; AAU86735.  
Nucleic acid encoding novel connective tissue associated polypeptides,  
used in diagnosing, preventing, treating or ameliorating a disorder such  
as cancer or rheumatoid arthritis.  
Claim 4; SEQ ID NO 311; 673pp; English.  
The present invention relates to the isolation of novel human connective  
tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide  
(CDNA and genomic) sequences encoding them. The sequences of the  
invention are useful in the diagnosis, treatment, prevention and/or  
prognosis of diseases associated with connective tissue(s), including  
cancer. The polynucleotide sequences of the invention are also useful in  
gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the  
novel human connective tissue related polypeptides. Note: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pat\_sequences  
Sequence 548 BP; 99 A; 154 C; 167 G; 121 T; 0 U; 7 Other;

Alignment Scores:  
Pred. No.: 2,47e-53 Length: 548  
Score: 639.00 Matches: 127  
Percent Similarity: 97.69% Conservative: 0  
Best Local Similarity: 97.69% Mismatches: 3  
Query Match: 58.95% Indels: 2  
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US-10-071-174-2 (1-204) x ABK41913 (1-548)

QY	75	PheGluLeuValAlaLeuMetAlaAspSerValLeuSerAspSerProGlyProThrTrp	94
DB	74	TTTCGAGCTGGTCGGCTGATGCGGATTCGCGTCTCCGACAGCCCGGCCACCTGG	133
QY	95	GlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuVal	114
DB	134	GC-AGAGTGGTACGCTCGTGACCTTCGACGAGGACGCTGCTGGAGAGGCGCTGGTG	192
QY	115	ThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGlnGluGlyAspVal	134
DB	193	ACCGCCCGTGAAGAAGTGGGCTTCACCGCGGCTAAAGGAGCAGGAGGCGCACGTC	252
QY	135	AlaArgAspCysGlnArgLeuValAlaLeuSerSerArgLeuMetGlyGlnHisArg	154
DB	253	GCSCGGAGCTGCAGCGCTGTCGCTGCTGAGCTCGGCTCATGGGCGAGCACCGG	312
QY	155	AlaTrpLeuGlnAlaGlnGlyTrpAspGlyPheCysHisPheArgThrProPhe	174
DB	313	CC-TGGCTCGAGCTCAGCGCGCTGGATGCTTTTGTCACTTCTTCAGGACCCCTTT	371
QY	175	ProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrThr	194
DB	372	CCACTGGCTTTTGGAGAAAAAGCTGGTGGCCAGGCTTTTCTGTCATGCTTGTAAACA	431
QY	195	AlaPheIleTrpLeuTrpThrArgLeuLeu	204

PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
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PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
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PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764847.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
PI  
XX  
XX WPI; 2003-634869/60.  
DR P-FSDB; ADB60069.  
XX  
PT New connective tissue-related polypeptides and polynucleotides, useful  
PT for treating, preventing and/or prognosing e.g. disorders of connective  
PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or  
PT neoplasias.  
XX  
PS Claim 1; SEQ ID NO 311; 248pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I), which  
CC comprises a sequence that is at least 95 % identical to a connective  
CC tissue-related polynucleotide encoding connective tissue antigens (CTA).  
CC The polypeptide or polynucleotide is useful for preventing, treating, or  
CC ameliorating medical conditions in a mammal. The connective tissue  
CC polypeptides, polynucleotides and antibodies are particularly useful for  
CC treating, preventing and/or prognosing disorders of connective tissues  
CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,  
CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or  
CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.  
CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases  
CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass  
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,  
CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.  
Alignment Scores:  
Pred. No.: 2,47e-53 Length: 548  
Score: 639.00 Matches: 127  
Percent Similarity: 97.69% Conservative: 0  
Best Local Similarity: 97.69% Mismatches: 3  
Query Match: 58.95% Indels: 2  
DB: 9 Gaps: 0  
US-10-071-174-2 (1-204) x ADB59580 (1-548)  
Qy 75 PhecluleuValAlaLeuMetAlaAspSerValIleuSerAspSerProGlyProThrTyr 94  
Db 74 TTCAGCTGGTGGCGCTGA\*GGCGGATTCGCTCTCCGACAGCCCGCCACCTGG 133

QY 95 GlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuVal 114  
 DB 134 GC-AGAGTGGTACGCTCGTACCTTCGACGGACCGCTCTGGAGAGAGCGCGTGTG 192  
 QY 115 ThrAlaArgTrpLysLysTrpGlyPheGlnProArgLeuLysGluGlnGlyAspVal 134  
 DB 193 ACCGCCGGTGGAGAGTGGGCTTCACGCCGGCTTAAGAGAGCAGAGGGCGACGTC 252  
 QY 135 AlaArgAspCysGlnArgLeuValAlaLeuLeuSerArgLeuMetGlyGlnHisArg 154  
 DB 253 GCCSGGACCTGCCAGGCCCTGGTGGCTTCTGAGCTCGGGCTCATGGGGAGACCGG 312  
 QY 155 AlaTrpLeuGlnAlaGlnGlyTrpAspGlyPheCysHisPhePheArgThrProPhe 174  
 DB 313 CC-TGGCTGCARGCTCAGGGCGCTGGATGGCTTTTGTCACTTCTCAGGACCGCCCTT 371  
 QY 175 ProLeuAlaPheTrpArgLysGlnLeuValGlnAlaPheLeuSerCysLeuLeuThrThr 194  
 DB 372 CCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTGTCATGCTGTTAACA 431  
 QY 195 AlaPheLeuTrpLeuTrpThrArgLeuLeu 204  
 DB 432 GCCTTCATTATCTCTGGACACGATTATTA 461

## RESULT 7

ABQ44403

ID ABQ44403 standard; DNA; 874 BP.

XX AC ABQ44403;

XX XX

XX 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30994.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX drug; side effect; cancer; central nervous system; cardiovascular;

XX gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for

XX diagnosis and prognosis, comprises selective hybridization of amplicons

XX from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of

XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a

XX genomic sample of DNA. The sample is treated chemically to convert

XX cytosine (C) but not methylated C, to uracil, then part of the genomic

XX DNA that contains the target C is amplified to form a labeled amplicon.

XX The amplicon is hybridised to two classes, each with at least one member,

XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the

XX degree of hybridisation to both classes is determined from the label on

XX the amplicon. From the ratio of labels hybridised to the two classes of

XX oligomers, the degree of methylation is calculated. The method is used;

XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs

CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

XX SQ Sequence 874 BP; 374 A; 291 C; 90 G; 119 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3,09e-45 Length: 874  
 Score: 559.00 Matches: 110  
 Percent Similarity: 83.75% Conservative: 24  
 Best Local Similarity: 68.75% Mismatches: 26  
 Query Match: 51.57% Indels: 0  
 DB: 6 Gaps: 0

US-10-071-174-2 (1-204) x ABQ44403 (1-874)

QY 1 MetValAspGlnLeuArgGluArgThrThrMetAlaAspProLeuArgGluArgThrGlu 20  
 DB 149 ATAATTAAACCAATTACGAAACCGCACCCACCACCAACCGCCGCTAGGAAACGCCAGAA 208  
 QY 21 LeuLeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40  
 DB 209 CTATTACTAACCGACTACTAAATAATCTAGCCCGGAAACCCGACACCCCGGAAACCGAG 268  
 QY 41 ProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHis 60  
 DB 269 CCATCCAGCCCGGAAACCGCGGTACTACGCTCGCGACCGCCCAATATACGACAAATCAC 328  
 QY 61 ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu 80  
 DB 329 CGATCCCTTTTCTCCGCTACCTCGACTACCCGAAACCGCTTCGAACCTAATAACGCTA 388  
 QY 81 MetAlaAspSerValLeuSerAspSerProGlyProThrTrpGlyArgValValThrLeu 100  
 DB 389 ATAACGAATCCGTACTCTCCGACACCCCGACCCCGCCCTAAACAAATAATATACGCTC 448  
 QY 101 ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTrpLysLys 120  
 DB 449 GTAACCTTCGCAAAACCGCTACTAAAAAATAACCGCTAATAACCGCCCGGATAAAAAA 508  
 QY 121 TrpGlyPheGlnProArgLeuLysGluGlnGlyAspValAlaArgAspCysGlnArg 140  
 DB 509 TAAAACTTCCACCGCGACTAAAAAATAACAAACGACGCGCCCGGAAACTACCAACGC 568  
 QY 141 LeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGln 160  
 DB 569 CTATAACCTTACTAAACTCGGACTCATATAACACACACCGCCGCTTAACCTACAACTCAA 628

## RESULT 8

ABQ44402/c

ID ABQ44402 standard; DNA; 874 BP.

XX AC ABQ44402;

XX 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 30993.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

XX drug; side effect; cancer; central nervous system; cardiovascular;

XX gastrointestinal; respiratory system; single nucleotide polymorphism;

XX SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.



07-MAR-2002.	426	GTAACCTTCGCAAAACGCTACTATAAAAAACCGCTAAATAACCGCCGTATAAAAAA	367
01-SEP-2001; 2001WO-BP010074.	121	TrpGlyPheGlnProArgLeuLysGluGlnGlyAspValAlaArgAspCysGlnArg	140
01-SEP-2000; 2000DE-01043826.	366	TAAACTTCACCGCGACTATAAAAAACAAACGAGCGTCCGCGAAGTACCAACGC	307
05-SEP-2000; 2000DE-01044543.	141	LeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGln	160
(EPIG-) EPIGENOMICS AG.	306	CTAATAACCTTACTAACTCGCGACTATAAAAAACACCGCGCTAATACTACAACTCAA	247
Olek A, Piepenbrock C, Berlin K, Guetig D;			
WPI; 2002-371829/40.			
Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.			
Claim 12; 56pp + Sequence Listing; 56pp; German.			
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous cardiovascular gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention			
Sequence 874 BP; 119 A; 90 C; 291 G; 374 T; 0 U; 0 Other;			
Alignment Scores:			
Pred. No.:	3.09e-45	Length:	874
Score:	559.00	Matches:	110
Percent Similarity:	83.75%	Conservative:	24
Best Local Similarity:	68.75%	Mismatches:	26
Query Match:	51.57%	Indels:	0
DB:	6	Gaps:	0
US-10-071-174-2 (1-204) x ABQ44402 (1-874)			
QY	1	MetValAspGlnLeuArgGluArgThrThrMetAlaAspProLeuArgGluArgThrGlu	20
Db	726	ATAATTACCAATTACGAAACGACCCACCATACCGCGCTACGAAACGACCGAA	667
QY	21	LeuLeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla	40
Db	666	CTATTACTACCGACTACCTAAATACTACGCGCGGAAACCGACACCCGACCGACG	607
QY	41	ProSerThrProGluAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnLeHis	60
Db	606	CCATCCAGCCCGGAACCCGCTACTACGCTCCGCGACCGCAATTCGACCAATTCAC	547
QY	61	ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu	80
Db	546	CGATCCCTTTTCTCCGCCCTACCTCGACTACCGCGGAAACCGCTTCGAACTAATACGCTA	487
QY	81	MetAlaAspSerValLeuSerAspSerProGlyProThrTrpTyrGlyArgValValThrLeu	100
Db	486	ATAACCAATTCGCTACTCTCCGACACCCCGACCCCACTTAAACAAATAATATACGCTC	427
QY	101	ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTrpLysLys	120

Pred. No.: 9,92e-41 Length: 874  
Score: 513.00 Matches: 111  
Percent Similarity: 69.33% Conservative: 2  
Best Local Similarity: 68.10% Mismatches: 50  
Query Match: 47.32% Indels: 0  
DB: 6 Gaps: 0

US-10-071-174-2 (1-204) x ABQ44405 (1-874)

QY 1 MetValAspGlnLeuArgGluArgThrMetAlaAspProLeuArgGluArgThrGlu 20  
DB 149 ATGTTGATAGTTCGGGAGCGTATTATTATGTCGATTCGTCGGGAGCGTATCGAG 208  
QY 21 LeuLeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40  
DB 209 TTGTTGTTGTCGATTTATTTGGGATATTCGTTCCGGAATTCGATATTTCCAGTCGGCG 268  
QY 41 ProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnLeHis 60  
DB 269 TTAATTTACGTTTCAGGTCGTCGTTGTCGTTTCGCGCGTTCGTTAGGTACGTTAGATTAT 328  
QY 61 ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu 80  
DB 329 CGTTTATTTTTCGTTATTTTCGTTATTTTCGGAATTCGTTTCGAGTTGTCGCGTTG 388  
QY 81 MetAlaAspSerValLeuSerAspSerProGlyProThrTyrGlyArgValValThrLeu 100  
DB 389 ATGCGGATTTTCGTTTTCGATGTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 448  
QY 101 ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTyrPheLys 120  
DB 449 GTGATTTTCGTTGAGGAGGTTGTTGGAGAGGTCGTTGTCGATCGTTCCGTTGGAAGAG 508  
QY 121 TrpGlyPheGlnProArgLeuLysGluGlnGluGlyAspValAlaArgAspCysGlnArg 140  
DB 509 TGGGTTTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 568  
QY 141 LeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGln 160  
DB 569 TTGTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 628  
QY 161 GlyGlyTrp 163  
DB 629 GCGGTTGG 637

RESULT 10

ABQ44405/c

ID ABQ44405 standard; DNA; 874 BP.

AC ABQ44405;

XX 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30996.

XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.

XX Homo sapiens.

XX W0200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074..

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-01044543.

XX (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and/or of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention

SQ Sequence 874 BP; 320 A; 320 C; 90 G; 144 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,92e-41 Length: 874  
Score: 513.00 Matches: 111  
Percent Similarity: 69.33% Conservative: 2  
Best Local Similarity: 68.10% Mismatches: 50  
Query Match: 47.32% Indels: 0  
DB: 6 Gaps: 0

US-10-071-174-2 (1-204) x ABQ44405 (1-874)

QY 1 MetValAspGlnLeuArgGluArgThrMetAlaAspProLeuArgGluArgThrGlu 20  
DB 726 ATGTTGATAGTTCGGGAGCGTATTATTATGTCGATTCGTCGGGAGCGTATCGAG 667  
QY 21 LeuLeuLeuAlaAspTyrLeuGlyTyrCysAlaArgGluProGlyThrProGluProAla 40  
DB 666 TTGTTGTTGTCGATTTATTTGGGATATTCGTTCCGGAATTCGATATTTTCGAGTCGGCG 607  
QY 41 ProSerThrProGluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnLeHis 60  
DB 606 TTAATTTACGTTTCAGGTCGTCGTTGTCGTTTCGCGCGTTCGTTAGGTACGTTAGATTAT 547  
QY 61 ArgSerPhePheSerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeu 80  
DB 546 CGGTTTTTTTTTCGTTTATTTTCGTTTATTTTCGGAATTCGTTTCGAGTTGTCGCGTTG 487  
QY 81 MetAlaAspSerValLeuSerAspSerProGlyProThrTyrGlyArgValValThrLeu 100  
DB 486 ATGCGGATTTTCGTTTTCGATAGTTTCGTTTATTTTCGCGGTAGAGTGGTACGTTTC 427  
QY 101 ValThrPheAlaGlyThrLeuLeuGluArgGlyProLeuValThrAlaArgTyrPheLys 120  
DB 426 GTGATTTTCGTTAGGACGTTTCGAGAGAGGTCGTTGTCGATCGTTCCGTCGGAAGAG 367  
QY 121 TrpGlyPheGlnProArgLeuLysGluGlnGluGlyAspValAlaArgAspCysGlnArg 140  
DB 366 TGGGTTTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTT 307  
QY 141 LeuValAlaLeuLeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGln 160





CC related physiological condition. An array of the invention is useful for  
CC determining mitochondrial biology gene expression profiles of organisms,  
CC such as human, mice and closely related species, tissue and organs of  
CC such organisms, which are useful for determining expression profiles  
CC diagnostic of energy metabolism-related physiological conditions,  
CC diagnosing such physiological conditions, identifying biochemical  
CC pathways, genes, and mutations involved in such physiological conditions,  
CC identifying therapeutic agents useful for preventing and/or treating such  
CC physiological conditions, evaluating and/or monitoring the efficacy of  
CC such therapies, and creating and identifying animal models of human  
CC energy metabolism-related physiological conditions. An array is also  
CC useful for defining expression signatures or profiles for mitochondrial  
CC diseases, as well as distinguishing clinical disorders that result from  
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,  
CC apoptosis and aging. An array of the invention contains probes of genes  
CC not previously recognised to participate in mitochondrial biology. The  
CC sequences shown in ADD33224-AD335260 represent murine mitochondrial DNA  
CC clones used to make the probes of the invention. Some sequences are not  
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,  
CC 1906, 2408 and 2643.

XX  
SQ Sequence 338 BP; 76 A; 95 C; 100 G; 67 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.7e-10 Length: 338  
Score: 199.00 Matches: 38  
Percent Similarity: 72.46% Conservative: 12  
Best Local Similarity: 55.07% Mismatches: 19  
Query Match: 18.36% Indels: 0  
DB: 10 Gaps: 0

US-10-071-174-2 (1-204) x ADD34583 (1-338)

QY 13 AspProLeuArgGluArgThrGluLeuLeuLeuAlaAspTyrLeuGlyTyrCysAlaArg 32  
Db 132 GACCCACTGCATGACGCACTAGACGGCTGCTGCTGACTACATATCTTCGCGACGG 191  
QY 33 GluProGlyThrProGluProAlaProSerThrProGluAlaValLeuArgSerAla 52  
Db 192 GAGCCGGACACCCGAGGACCCGCGCCACGCTGCTGCGGGCGCCTTGCTTCGCTGTG 251  
QY 53 AlaAlaArgLeuArgGlnIleHisArgSerPheSerAlaTyrLeuGlyTyrProGly 72  
Db 252 ACTAGGCAGATCCAGCAGGAGCACCAGAAATTTTCTCTCTCTGCGAAGCCGGGGC 311  
QY 73 AsnArgPheGluLeuValAlaLeuMet 81  
Db 312 AATCGCTGAGCTGCTGTAACACAGATG 338

RESULT 14

ABT09344  
ID ABT09344 standard; DNA; 658 BP.  
XX  
AC ABT09344;  
XX  
XX 05-DEC-2002 (first entry)  
XX  
DE Phase-1 Rat CT gene SEQ ID No 432.  
XX  
XX Rat; toxicity study; rat toxic response gene; toxicological response;  
KW drug development; Phase-1 rat CT gene; ds.  
XX  
XX Rattus sp.  
XX  
XX W020026682-A2.  
XX  
XX 29-AUG-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002935.  
XX  
XX 29-JAN-2001; 2001US-0264933P.  
PR 26-JUL-2001; 2001US-0308161P.  
XX

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

PA Farris G, Hicken SH, Farr SB;

XX WPI; 2002-674961/72.

XX Evaluating the toxicity of an agent, useful in drug development or in  
XX determining toxicological responses to a new drug, by determining the  
XX expression of rat toxicologically relevant genes in the test animal in  
XX response to the test agent.

PS Disclosure; Page 213; 38pp; English.

XX The invention relates to a method used for evaluating the toxicity of an  
XX agent comprising determining the expression of a rat toxic response  
XX gene(s) in the test animal in response to the agent. The method is useful  
XX in drug development, particularly for conducting toxicity studies and  
XX analysis before a new drug or compound is approved for human consumption  
XX or use. The method is also useful in determining toxicological responses  
XX to a new drug. This polynucleotide sequence represents a phase-1 rat CT  
XX gene of the invention

SQ Sequence 658 BP; 138 A; 178 C; 194 G; 147 T; 0 U; 1 Other;

Alignment Scores:  
Pred. No.: 0.00287 Length: 658  
Score: 129.00 Matches: 58  
Percent Similarity: 37.44% Conservative: 24  
Best Local Similarity: 26.48% Mismatches: 75  
Query Match: 11.90% Indels: 62  
DB: 6 Gaps: 12

US-10-071-174-2 (1-204) x ABT09344 (1-658)

QY 8 ArgThrThrMetAlaAspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeu 27  
Db 51 GCGAGTGTGCTGAATTCGCCCTTCGCGGAATTCGGGCCCTTTTGTACAGGGTTTCATC 110  
QY 28 ---GlyTyrCysAlaArgGluProGly---ThrProGlu---ProAlaProSerThrPro 44  
Db 111 CAGGATCGAGCAGAGAGATGGCTGGGGGAGACACCTGAGCTGACCTTGGAGCAGCCGCC 170  
QY 45 GluAlaAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHisArgSerPhePhe 64  
Db 171 CAGACGCATCCACCAAGAGAGCTGAGCGAGTGTCTCAGGGCAATTCGGCGATGAATG 227  
QY 65 SerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeuMetAlaAspSer 84  
Db 228 -----GACAAACACATGAGCTGCAGAGGATGATGCTGAT--- 263  
QY 85 ValLeuSerAspSerProGlyPro----- 92  
Db 264 GTGGATACAGACTCCCGCCGAGAGGTCTTCTCGTGTGGCAGCTGACATGTTTGCAGAC 323  
QY 93 -----ThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGlu 109  
Db 324 GGCAACTTCAACTGGGCGGGTGGTGGCTTTCTACTTTGCTAGCAAACTGGTGCTC 383  
QY 110 Arggly-----ProLeuValThrAlaArgTrpIlyLysTrpGlyPheGln 124  
Db 384 AAGCCCTGTGCTACTAAAGTCCCGAGCTGATCAGAACCATCATGGCTGG----- 434  
QY 125 ProArgLeuLysGluGlnGluGlyAspValAlaArgAspCysGlnArgLeuValAlaLeu 144  
Db 435 -----ACATGGACTTC 446  
QY 145 LeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyGlyTrpAsp 164  
Db 447 CTCGGGAGCGGCTGCTT-----GTCTGGATCCCAAGACCGAGGTGGCTGGAT 494  
QY 165 GlyPheCysHisPhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuVal 184  
Db 495 GGCCTCTCTTCTACTTCGGGACCCCG-----ACATGG-----CAGACATG 536

**Qy** 185 GlnAlaPheLeuSerCysLeuLeuThrThrAlaPheIleTyrLeuTrpThrArgLeu 203  
|||::: ||| |::: ||| |::: ||| |::: |||  
**Db** 537 ACCATCTTTGGCGGAGTCCT---ACTGCCTCGGTACCATCTCGAAGAAGCTT 590

RESULT 15

ADG30848  
ID ADG30848 standard: DNA: 658 BP.

AC ADG30848:

DT 26-FEB-2004 (first entry)

DE Liver toxicity predictive DNA 28.

liver toxicity: Norway rat; 24 hour combo All: ds.

Unidentified.

AA PN WO2003085083-A2.

XX  
PD  
16-OCT-2003XX  
PF  
01-APR-2003: 2003WO-US010141.01-APR-2002: 2002US-0369287P-XX  
PR

XX (PHAS-) PHASE 1 MOLECULAR TOXICOLOGY.

PI Kier L. Nolan TD. Sankar U. Derbel M:

AA  
DR WPI; 2003-804300/75.

Predicting the liver toxicity of an agent to an individual by using the test expression profile with a set of reference expression profiles in a Predictive Model to determine whether the agent will reduce liver toxicity in the individual.

PS Claim 2: Page 153: 379pp: English:

The invention relates to a novel method for predicting the liver toxicity of an agent to an individual comprising obtaining a biological sample from an individual treated with the agent, measuring the expression of one or more liver toxicity predictive genes in the sample and using the test expression profile with a set of reference expression profiles in a predictive model to determine whether the agent will reduce liver toxicity in the individual. The method of the invention may be useful for predicting the liver toxicity of an agent to an individual. The current sequence is that of the liver toxicity predictive DNA of the invention which represents a 24 hour combo All gene.

Sequence 658 BP; 138 A; 178 C; 194 G; 147 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	0.00287	Length:	658
Score:	129.00	Matches:	58
Percent Similarity:	37.44%	Conservative:	24
Best Local Similarity:	26.48%	Mismatches:	75
Query Match:	11.90%	Indels:	62
DB:	10	Gaps:	12

US-10-071-174-2 (1-204) x ADG30848 (1-658)

QY 8 ArgThrThrMetAlaAspProLeuArgGluArgThrGluLeuLeuAlaAspTyrLeu 27

Db 51 CGCAGTGTGCTGAATTCCGCCCTTCGCGGAATTCGGGGCCCTTTTGTACAGGGTTTCATC 110

Qy 28 ---GlyTyrCysAlaArgGluProGly---ThrProGlu---ProAlaProSerThrPro 44

Db 111 CAGGATCGAGCAGAGAGGATGGCTGGGGAGACACCTGAGCTGACCTTGGAGCAGCCGCC 170

Qy 45 GluAlaValLeuArgSerAlaAlaAlaArgLeuArgGlnIleHisArgSerPhe 64

171	Db	CAGGACGATCCACCAAGAACTGAGCGAGTGCTCTCAGGCGAATTGGCGATGAACTG---222
65	Qy	SerAlaTyrLeuGlyTyrProGlyAsnArgPheGluLeuValAlaLeuMetalAlaAspSer84
228	Db	-----GACAAACAATGGAGCTGCAGAGGATGATTGCTGTAT---263
85	Qy	ValLeuSerAspSerProGlyPro-----92
264	Db	GTGGATACAGACTCCCCCGAGAGGCTTCTTCGTGTGCGACTGACATGTTTGCAGAC323
93	Qy	-----ThrTrpGlyArgValValThrLeuValThrPheAlaGlyThrLeuLeuGlu109
324	Db	GGCAACTCAACTGGGGCGGGTGGTTCCTTTCTACTTGTACAAACTGGTGCTC383
110	Qy	ArgGly-----ProLeuValThrAlaArgTrpIysIysTrpGlyPheGln124
384	Db	AAAGGCCCTGTGCACCTAAAGTCCCGAGCTGATCAGAACCATCATGGCTGG-----434
125	Qy	ProArgLeuLysGluGlnGluGlyAspValAlaArgAspCysGlnArgLeuValAlaLeu144
435	Db	-----ACACTGGCACTTC446
145	Qy	LeuSerSerArgLeuMetGlyGlnHisArgAlaTrpLeuGlnAlaGlnGlyTrpAsp164
447	Db	CTCCGGGAGCGGCTGCTT-----GTCTGGATCCAAGACACCGGGTGGCTGGAT494
165	Qy	GlyPheCysHisPhePheArgThrProPheProLeuAlaPheTrpArgLysGlnLeuVal184
495	Db	GGCCCTCTTCTCCTCTCGGACCCCC-----ACATGG-----CAGACAGTGG536
185	Qy	GlnAlaPheLeuSerCysLeuLeuThrThrAlaPheIleTyrLeuTrpThrArgLeu203
537	Db	ACCATCTTTGGCTGGAGTCCCTC-----ACTGCTCTGCTCACCCTCGGAAGACCT590

Search completed: November 7, 2004, 06:26:07  
Job time : 514 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 01:20:07 ; Search time 6234 seconds  
(without alignments)  
6728.579 Million cell updates/sec

Title: US-10-071-174-1

Perfect score: 887

Sequence: 1 cgggccaagaaaccagcga.....ctctctcttgagtgaagaa 887

Scoring table: -OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_intg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	100.0	887	9 AF326964	AF326964 Homo sapi
2	763	86.0	1168	6 BD233466	BD233466 Human pro
3	615	69.3	615	9 AF285032	AF285032 Homo sapi
4	585	66.0	585	9 HS458330	AJ458330 Homo sapi
5	582	65.6	582	6 BD233456	BD233456 Human pro
C 6	539	60.8	93287	9 AC023906	AC023906 Homo sapi
7	439	49.5	726	6 CQ752105	CQ752105 Sequence
C 8	267	30.1	214669	2 AC018903	AC018903 Homo sapi
9	60	6.8	60	6 CQ545914	CQ545914 Sequence
10	47	5.3	214669	2 AC018903	AC018903 Homo sapi
C 11	22	2.5	5147	6 BD183336	BD183336 Novel gen
C 12	22	2.5	5147	6 BD171150	BD171150 Novel gen
C 13	22	2.5	5147	9 AB051441	AB051441 Homo sapi
14	22	2.5	21560	9 AY245248	AY245248 Homo sapi
15	22	2.5	60828	9 HS1191B2	AL022237 Human DNA
C 16	22	2.5	277861	2 HSAC000406	BC030863 Homo sapi
17	21	2.4	3011	10 BC030863	BC030863 Homo sapi
18	21	2.4	4353	10 AK173033	AK173033 Mus muscu
19	21	2.4	6190	10 BC043122	BC043122 Mus muscu

C 20	21	2.4	13635	1 AE005068	AE005068 Halobacte
C 21	21	2.4	95178	2 AL391556	AL391556 Homo sapi
C 22	21	2.4	120311	10 AC006945	AC006945 Mus muscu
23	21	2.4	155300	2 AL929459	AL929459 Danio rer
C 24	21	2.4	163574	2 AC138826	AC138826 Homo sapi
25	21	2.4	167273	10 AC083894	AC083894 Mus muscu
C 26	21	2.4	172144	2 AC136529	AC136529 Rattus no
C 27	21	2.4	172997	9 AC117516	AC117516 Homo sapi
C 28	21	2.4	190189	2 AC027181	AC027181 Homo sapi
C 29	21	2.4	224038	10 AL732625	AL732625 Mouse DNA
C 30	21	2.4	226457	2 AC127098	AC127098 Rattus no
C 31	21	2.4	231546	2 AC125302	AC125302 Rattus no
32	21	2.4	238290	2 AC112431	AC112431 Rattus no
33	21	2.4	288494	2 AC111749	AC111749 Rattus no
C 34	21	2.4	316892	2 AC096101	AC096101 Rattus no
C 35	20	2.3	284	11 G47512	G47512 Z25086.1 Ze
36	20	2.3	823	6 CQ780061	CQ780061 Sequence
37	20	2.3	823	6 CQ782081	CQ782081 Sequence
38	20	2.3	823	6 BD124770	BD124770 Primer fo
39	20	2.3	823	6 BD126790	BD126790 Primer fo
40	20	2.3	1134	8 AK066814	AK066814 Oryza sat
41	20	2.3	1209	10 AF102501	AF102501 Mus muscu
42	20	2.3	1225	10 AF067660	AF067660 Mus muscu
43	20	2.3	1257	10 BC052690	BC052690 Mus muscu
C 44	20	2.3	1672	9 AY167728	AY167728 Porogo pyg
45	20	2.3	38674	9 HSU81831	U81831 Human cosmi

ALIGNMENTS

RESULT 1 AF326964 887 bp mRNA linear PRI 01-MAY-2001  
LOCUS Homo sapiens BCLB (BCLB) mRNA, complete cds.  
DEFINITION AF326964  
ACCESSION AF326964.1 GI:13898393  
VERSION AF326964.1  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 887)  
AUTHORS Ke,N., Godzik,A. and Reed,J.C.  
TITLE Bcl-B, a novel Bcl-2 family member that differentially binds and regulates Bax and Bak  
J. Biol. Chem. 276 (16), 12481-12484 (2001)  
JOURNAL MEDLINE  
PUBMED 21201065  
REFERENCE 2 (bases 1 to 887)  
AUTHORS Ke,N., Godzik,A. and Reed,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-2000) The Burnham Institute, 10901 N. Torrey Pines Rd., La Jolla, CA 92037, USA  
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Db 1	CGGGCCAGAAACACAGCGAAGCCCGCGCCCGCCAGACAGAGGCCGACCATGGTTGACCA	60		
Qy 61	GTTCGGGAGCGCACCAATGGCCGACCCGCTGCGGGAGCGCACCGAGCTTTTCTGCTGC	120		
Db 61	GTTCGGGAGCGCACCAATGGCCGACCCGCTGCGGGAGCGCACCGAGCTTTTCTGCTGC	120		
Qy 121	CGACTACTGGGGTACTCGGCCCGGGAAACCGGCACCCCGAGCGCGGCCCATCCACGCC	180		
Db 121	CGACTACTGGGGTACTCGGCCCGGGAAACCGGCACCCCGAGCGCGGCCCATCCACGCC	180		
Qy 181	CGAGGCGCGCTGCTGCCTCCGCGGCGCGCAGGTTACGGCAGATTCAACCGTCTCTTTT	240		
Db 181	CGAGGCGCGCTGCTGCCTCCGCGGCGCGCAGGTTACGGCAGATTCAACCGTCTCTTTT	240		
Qy 241	CTCCGGCTACTCTGGCTACCCGGGAAACCGCTTCGAGCTTGTGGCGCTCATCGCGGATC	300		
Db 241	CTCCGGCTACTCTGGCTACCCGGGAAACCGCTTCGAGCTTGTGGCGCTCATCGCGGATC	300		
Qy 301	CGTGTCTCCGACAGCCCCCGCCACCTGCGGGCAGAGTGGTGACGCTCGTGACCTTCGC	360		
Db 301	CGTGTCTCCGACAGCCCCCGCCACCTGCGGGCAGAGTGGTGACGCTCGTGACCTTCGC	360		
Qy 361	AGGAGCGCTGTGGAGAGAGGCGCTGTTGACCGCCGCTGGAAGAGTGGGGCTTCCA	420		
Db 361	AGGAGCGCTGTGGAGAGAGGCGCTGTTGACCGCCGCTGGAAGAGTGGGGCTTCCA	420		
Qy 421	GCCCGGCTTAAAGAGACAGAGGCGCGAGCTCGCCCGGGGACTGCGACGCGCTGTGGCCCTT	480		
Db 421	GCCCGGCTTAAAGAGACAGAGGCGCGAGCTCGCCCGGGGACTGCGACGCGCTGTGGCCCTT	480		
Qy 481	GCTGAGCTCGCGCTCATGGGGCAGACCGCGCTGCTCGAGCTCAGGGCGGCTGGGA	540		
Db 481	GCTGAGCTCGCGCTCATGGGGCAGACCGCGCTGCTCGAGCTCAGGGCGGCTGGGA	540		
Qy 541	TGGCTTTTGTCACTTCTTCAGACCCCCCTTCCACTGGCTTTTGGAGAAAACAGCTGT	600		
Db 541	TGGCTTTTGTCACTTCTTCAGACCCCCCTTCCACTGGCTTTTGGAGAAAACAGCTGT	600		
Qy 601	CCAGGCTTTTCTGTCATGCTTTTAAACAGAGCTTCATTATCTCTGACACGATTATT	660		
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Db 661	ATGAGTTTTAAACCTTTTAAACCGGCTCTTACTGCCCAACTGTGACCAATAATGACAG	720		
Qy 721	ATGTGTGAAACAAGAACTGAGGGAAAGCACTTCCGCCACCCGACAGCTTTTATCTGA	780		
Db 721	ATGTGTGAAACAAGAACTGAGGGAAAGCACTTCCGCCACCCGACAGCTTTTATCTGA	780		
Qy 781	ATGCATACAGAGAGTCTCGAGTGTGTGATTTGGCCAGTGTTTTAACTTGTGACAGTACT	840		
Db 781	ATGCATACAGAGAGTCTCGAGTGTGTGATTTGGCCAGTGTTTTAACTTGTGACAGTACT	840		
Qy 841	CAGGTGTGAGGCAAGAAATGCAATGGCTCTTCCTTGTAGTGAAGAA	887		
Db 841	CAGGTGTGAGGCAAGAAATGCAATGGCTCTTCCTTGTAGTGAAGAA	887		

RESULT 2					
BD233466					
LOCUS	BD233466	1168 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Human protein having hydrophobic domain and DNA encoding the same.				
ACCESSION	BD233466				

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BD233456.1  GI:33043236
JP 2002519016-A/12.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1168)
Kato, S. and Kimura, T.
Human protein having hydrophobic domain and DNA encoding the same
Patent: JP 2002519016-A 12 02-JUL-2002.
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS Homo sapiens (human)
FN JP 2002519016-A/12
PD 02-JUL-2002
PF 18-JUN-1999 JP 2000557267
PI SEISHI KATO, TOMOKO KIMURA
PC
C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N15/10, C12N15/00, C12N5/PC
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CC Human protein having hydrophobic domain and DNA encoding the
CC same
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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DB	481	TTCTTCAGGACCCCTTTTCCACTGGCTTTTGGAGAAAACAGCTGTGCCAGGCTTTCTG	540
QY	614	TCAAGCTGTTAACACAGCCTTCATTATCTCTGGACACGATTATTATGAGTTTAAAA	673



Db	541	TCATGCTGTTTAAACACAGCCTTCATTATCTCTGAGACGATTATATGAGTTTAAAA	600
Qy	674	CTTTTAAACCGCTTCTACCTGCCCACTGTGACAACTAATGACAGATGTGTGAGAAC	733
Db	601	CTTTTAAACCGCTTCTACCTGCCCACTGTGACAACTAATGACAGATGTGTGAGAAC	660
Qy	734	AGAACTGAGGGAAGACACCTTCCCAACCCAGACGTTTTTATCTCAATGATACAAAGGA	793
Db	661	AGAACTGAGGGAAGACACCTTCCCAACCCAGACGTTTTTATCTCAATGATACAAAGGA	720
Qy	794	GTCTGAGGTGGTGAATTTGTCAGTGTGTTTAACTTGTGACAAAGTACTCAGGTGTGAGGAC	853
Db	721	GTCTGAGGTGGTGAATTTGTCAGTGTGTTTAACTTGTGACAAAGTACTCAGGTGTGAGGAC	780
Qy	854	AGAACTGCAATGGCTCTTCCCTTGTGAGTGAAGAA	887
Db	781	AGAACTGCAATGGCTCTTCCCTTGTGAGTGAAGAA	814
RESULT 3			
LOCUS	AF285092	615 bp mRNA linear	PRI 08-NOV-2001
DEFINITION	Homo sapiens Bcl-2-like protein 10 mRNA, complete cds.		
ACCESSION	AF285092		
VERSION	AF285092.1	GI:9837265	
KEYWORDS	Homo sapiens (human)		
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Zhang, H., Holmgren, W. and De Geyter, C.		
AUTHORS	Bcl2-L-10, a novel anti-apoptotic member of the Bcl-2 family, blocks apoptosis in the mitochondria death pathway but not in the death receptor pathway		
TITLE	Hum. Mol. Genet. 10 (21), 2329-2339 (2001)		
JOURNAL	21548034		
MEDLINE	11689480		
PUBMED	Direct Submission		
AUTHORS	Zhang, H.H.		
TITLE	Submitted (05-JUL-2000) University Women's Hospital, Schanzentra		
JOURNAL	46, Basel 4057, Switzerland		
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Query Match	Best Local Similarity 100.0%; Pred. No. 0;		
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Qy	50	ATGTTTACAGTTCGGGAGCGCACCAACCATGGCCACCCCTCGGGAGCGCACCCAG	109
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Qy	110	CTGTTGCTGGCGGACTTACCTGGGTACTGCGCCCGGGAAACCGGACCCCGGCGG	169
Db	61	CTGTTGCTGGCGGACTTACCTGGGTACTGCGCCCGGGAAACCGGACCCCGGCGG	120

Qy	170	CCATCCAGCCCGAGCGCGCTGCTGGCTCCGCGCGCCAGGTTACGCGAGATTCAC	229
Db	121	CCATCCAGCCCGAGCGCGCTGCTGGCTCCGCGCGCCAGGTTACGCGAGATTCAC	180
Qy	230	CGGTCTTTTCTCGCTACCTCGGTACCCCGGACCGCTTCGAGCTGGTGGCGCTG	289
Db	181	CGGTCTTTTCTCGCTACCTCGGTACCCCGGACCGCTTCGAGCTGGTGGCGCTG	240
Qy	290	ATGGCGGATTCGCTGCTCCGACAGCCCCCGCCACCTCGGGCAGAGTGGTCAAGCTC	349
Db	241	ATGGCGGATTCGCTGCTCCGACAGCCCCCGCCACCTCGGGCAGAGTGGTCAAGCTC	300
Qy	350	GTGACCTTCGAGGAGCGTCTCGTGGAGAGAGGCGCTGTGTACCGCCCGTGAAGAAG	409
Db	301	GTGACCTTCGAGGAGCGTCTCGTGGAGAGAGGCGCTGTGTACCGCCCGTGAAGAAG	360
Qy	410	TGGGCTTCACAGCCCGCTAAAGAGCAGGAGGCGCAGCTCGCCCGGACTGCACGCG	469
Db	361	TGGGCTTCACAGCCCGCTAAAGAGCAGGAGGCGCAGCTCGCCCGGACTGCACGCG	420
Qy	470	CTGTGGCTTCGTGAGCTCGCGCTCATGGGGCAGCAGCGCGCTGGCTGCAAGCTCAG	529
Db	421	CTGTGGCTTCGTGAGCTCGCGCTCATGGGGCAGCAGCGCGCTGGCTGCAAGCTCAG	480
Qy	530	GGCGCTGGGATGCTTTTGTCACTTTCAGGACCCCTTCACCTGGCTTTTGAGA	589
Db	481	GGCGCTGGGATGCTTTTGTCACTTTCAGGACCCCTTCACCTGGCTTTTGAGA	540
Qy	590	AAACAGCTGGTCCAGGCTTTTCTGTCATGCTTTTAAACAGCCTTCATTTATCTCG	649
Db	541	AAACAGCTGGTCCAGGCTTTTCTGTCATGCTTTTAAACAGCCTTCATTTATCTCG	600
Qy	650	ACAGATTTATATGA	664
Db	601	ACAGATTTATATGA	615
RESULT 4			
LOCUS	HSA458330	585 bp DNA linear	PRI 25-APR-2002
DEFINITION	Homo sapiens NRH gene for anti-apoptotic protein.		
ACCESSION	AJ458330		
VERSION	AJ458330.1	GI:20338765	
KEYWORDS	anti-apoptotic protein; NRH gene.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1		
TITLE	Acouacheria, A., Arnaud, E., Venet, S., Lalle, P., Gouy, M., Rigal, D. and Gillet, G.		
JOURNAL	Nrh, a human homologue of Nr-13 associates with Bcl-Xs and is an inhibitor of apoptosis		
MEDLINE	Oncogene 20 (41), 5846-5855 (2001)		
PUBMED	21477277		
REFERENCE	2 (bases 1 to 585)		
AUTHORS	Gillet, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-2002) Gillet G., Ibcp, CNRS UMR 5086, 7 PASSAGE		
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Best Local Similarity 100.0%; Pred. No. 0;
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DB 1 ATGGCCGACCCGCTGGGGAGCGCACCGAGCTGTGCTGGCCGACTACCTGGGGTACTGC 60

QY 140 GCCCGGGAACCCGACCCCGGAGCGCGCCATCCACCGCCGAGCGCGCGCTGTGCGC 199
DB 61 GCCCGGGAACCCGACCCCGGAGCGCGCCATCCACCGCCGAGCGCGCGCTGTGCGC 120

QY 200 TCGCGGCGCCGAGGTACGGGAGATTCACCGGTCTCTTTCTCGCCCTACCTCGGCTAC 259
DB 121 TCGCGGCGCCGAGGTACGGGAGATTCACCGGTCTCTTTCTCGCCCTACCTCGGCTAC 180

QY 260 CCCGGGAACCCGCTTCGAGCTGTGGGCTGATGGCGGATTCGCTGTCTCCGACAGCCCC 319
DB 181 CCCGGGAACCCGCTTCGAGCTGTGGGCTGATGGCGGATTCGCTGTCTCCGACAGCCCC 240

QY 320 GGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTCGAGGAGCGCTGTGGAGAGA 379
DB 241 GGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTCGAGGAGCGCTGTGGAGAGA 300

QY 380 GGGCGCTGTGTGACCGCGCGTGGAGAGTGGGGCTTCAGCGCGCGCTAAAGGAGCAG 439
DB 301 GGGCGCTGTGTGACCGCGCGTGGAGAGTGGGGCTTCAGCGCGCGCTAAAGGAGCAG 360

QY 440 GAGGGCACTGTGCGCGGAGCTGACGCGCTGTGGGCTTCAGCGCGCGCTAAAGGAGCAG 499
DB 361 GAGGGCACTGTGCGCGGAGCTGACGCGCTGTGGGCTTCAGCGCGCGCTAAAGGAGCAG 420

QY 500 GGGCAGACCGCGCTGCTGCGAGCTCAGCGCGCTGGGATGGCTTTGTCACTTCTTC 559
DB 421 GGGCAGACCGCGCTGCTGCGAGCTCAGCGCGCTGGGATGGCTTTGTCACTTCTTC 480

QY 560 AGGACCCCTTTTCACTGGCTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGC 619
DB 481 AGGACCCCTTTTCACTGGCTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGC 540

QY 620 TTGTTAAACAACAGCCTTCATTTATCTCTGGACAGATTATTA 664
DB 541 TTGTTAAACAACAGCCTTCATTTATCTCTGGACAGATTATTA 585
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## RESULT 5

BD233456  
LOCUS Human protein having hydrophobic domain and DNA encoding the same.  
DEFINITION  
BD233456  
ACCESSION  
BD233456.1 GI:33043226  
VERSION  
KEYWORDS JP 2002519016-A/2.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 582)  
Kato, S. and Kimura, T.  
Human protein having hydrophobic domain and DNA encoding the same  
Patent: JP 2002519016-A 2 02-JUL-2002;  
TITLE  
JOURNAL SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

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COMMENT OS Homo sapiens (human)
PN JP 2002519016-A/2
PD 02-JUL-2002
PF 18-JUN-1999 JP 2000557267
PI SEISHI KATO, TOMOKO KIMURA
PC
C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N5/10, C12N15/00, C12N5/ PC
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CC same
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FEATURES
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ORIGIN
Query Match      65.6%; Score 582; DB 6; Length 582;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ATGGCCGACCCGCTGGGGAGCGCACCGAGCTGTGCTGGCCGACTACCTGGGGTACTGC 139
DB 1 ATGGCCGACCCGCTGGGGAGCGCACCGAGCTGTGCTGGCCGACTACCTGGGGTACTGC 60

QY 140 GCCCGGGAACCCGACCCCGGAGCGCGCCATCCACCGCCGAGCGCGCGCTGTGCGC 199
DB 61 GCCCGGGAACCCGACCCCGGAGCGCGCCATCCACCGCCGAGCGCGCGCTGTGCGC 120

QY 200 TCGCGGCGCCGAGGTACGGGAGATTCACCGGTCTCTTTCTCGCCCTACCTCGGCTAC 259
DB 121 TCGCGGCGCCGAGGTACGGGAGATTCACCGGTCTCTTTCTCGCCCTACCTCGGCTAC 180

QY 260 CCCGGGAACCCGCTTCGAGCTGTGGGCTGATGGCGGATTCGCTGTCTCCGACAGCCCC 319
DB 181 CCCGGGAACCCGCTTCGAGCTGTGGGCTGATGGCGGATTCGCTGTCTCCGACAGCCCC 240

QY 320 GGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTCGAGGAGCGCTGTGGAGAGA 379
DB 241 GGCCCACTTGGGGAGAGTGTGACGCTGTGACCTTCGAGGAGCGCTGTGGAGAGA 300

QY 380 GGGCGCTGTGTGACCGCGCGTGGAGAGTGGGGCTTCAGCGCGCGCTAAAGGAGCAG 439
DB 301 GGGCGCTGTGTGACCGCGCGTGGAGAGTGGGGCTTCAGCGCGCGCTAAAGGAGCAG 360

QY 440 GAGGGCACTGTGCGCGGAGCTGACGCGCTGTGGGCTTCAGCGCGCGCTAAAGGAGCAG 499
DB 361 GAGGGCACTGTGCGCGGAGCTGACGCGCTGTGGGCTTCAGCGCGCGCTAAAGGAGCAG 420

QY 500 GGGCAGACCGCGCTGCTGCGAGCTCAGCGCGCTGGGATGGCTTTGTCACTTCTTC 559
DB 421 GGGCAGACCGCGCTGCTGCGAGCTCAGCGCGCTGGGATGGCTTTGTCACTTCTTC 480

QY 560 AGGACCCCTTTTCACTGGCTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGC 619
DB 481 AGGACCCCTTTTCACTGGCTTTTGGAGAAAACAGCTGGTCCAGGCTTTTCTGTCATGC 540

QY 620 TTGTTAAACAACAGCCTTCATTTATCTCTGGACAGATTATTA 661
DB 541 TTGTTAAACAACAGCCTTCATTTATCTCTGGACAGATTATTA 582
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## RESULT 6

AC023906/c  
AC023906  
LOCUS Homo sapiens chromosome 15 clone CTD-2184D3 map 15q21.2, complete  
DEFINITION  
AC023906  
ACCESSION  
AC023906.7 GI:14595770  
VERSION  
KEYWORDS HTG.





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31814 31913: gap of unknown length
31914 33056: contig of 1143 bp in length
33057 33156: gap of unknown length
33157 34007: contig of 851 bp in length
34008 34107: gap of unknown length
34108 35200: contig of 1213 bp in length
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35421 36207: contig of 787 bp in length
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36309 37521: contig of 1214 bp in length
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38421 39260: gap of unknown length
39261 39826: gap of unknown length
39827 40635: contig of 809 bp in length
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40736 41845: contig of 1110 bp in length
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44019 44825: contig of 808 bp in length
44826 44925: gap of unknown length
44926 46114: contig of 1189 bp in length
46115 46214: gap of unknown length
46215 47131: contig of 817 bp in length
47132 48292: contig of 1161 bp in length
48293 48392: gap of unknown length
48393 49176: contig of 784 bp in length
49177 49276: gap of unknown length
49277 50889: contig of 1113 bp in length
50890 50489: gap of unknown length
50490 51333: contig of 844 bp in length
51334 51433: gap of unknown length
51434 52765: contig of 1332 bp in length
52766 52865: gap of unknown length
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57559 57858: gap of unknown length
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59846 60655: contig of 810 bp in length
60656 60755: gap of unknown length
60756 61976: contig of 1221 bp in length
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62077 62896: contig of 820 bp in length
62897 62997: gap of unknown length
62997 64128: contig of 1132 bp in length
64129 64229: gap of unknown length
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65027 65126: gap of unknown length
65127 66269: contig of 1143 bp in length
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71548 71647: gap of unknown length
71648 73629: contig of 1982 bp in length
73630 74587: contig of 858 bp in length
74588 75780: contig of 1093 bp in length
75781 75880: gap of unknown length
75881 77196: contig of 1316 bp in length
77197 78651: contig of 1355 bp in length
78652 78751: gap of unknown length
78752 79557: contig of 806 bp in length
79558 79657: gap of unknown length
79658 80774: contig of 1117 bp in length
80775 80874: gap of unknown length
80875 81690: contig of 816 bp in length
81691 81791: gap of unknown length
81792 82928: contig of 1138 bp in length
82929 83028: gap of unknown length
83029 83902: contig of 874 bp in length
83903 84002: gap of unknown length
84003 85193: contig of 1191 bp in length
85194 85293: gap of unknown length
85294 86149: contig of 856 bp in length

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30.1%; Score 267; DB 2; Length 214669;
BestLocal Similarity 100.0%; Pred.No 8.3e-141; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

QY 621 TGTTACACAGCCTTCATTATCTCTGGACACGATTATTATGAGTTTAAAACTTTTAA 680
Db 168497 TGTTACACAGCCTTCATTATCTCTGGACACGATTATTATGAGTTTAAAACTTTTAA 168438

QY 681 CCGCTTCTACCTGCCCACTGTGACCACTAATGACAGATGTGTGAGCAAGCACTG 740
Db 168437 CCGCTTCTACCTGCCCACTGTGACCACTAATGACAGATGTGTGAGCAAGCACTG 168378

QY 741 AGGAAAGCACCTTCCCCACCCAGACGTTTATCTGAATGACATACAGGAGTCTCTGA 800
Db 168377 AGGAAAGCACCTTCCCCACCCAGACGTTTATCTGAATGACATACAGGAGTCTCTGA 168318

QY 801 GGTGCTGATTGGCCAGTGTTTAACTTGACAACTACTCAGTGTGAGGACAAAGATG 860
Db 168317 GGTGCTGATTGGCCAGTGTTTAACTTGACAACTACTCAGTGTGAGGACAAAGATG 168258

QY 861 CAAATGCTCTTCTCTGAGTGAAGAA 887
Db 168257 CAAATGCTCTTCTCTGAGTGAAGAA 168231

RESULT 9
COS45914 COS45914 60 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 15549 from Patent WO0210449.
DEFINITION COS45914
ACCESSION COS45914
VERSION COS45914.1 GI:41512178
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 15549 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 CCCTTTCCACTGGCTTTTGGAGAAAACAGCTGTGTCAGGCTTTTCGTGTCATGCTTGT 624
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Db 1 CCCTTTCCACTGGCTTTTGGAGAAAACAGCTGTGTCAGGCTTTTCGTGTCATGCTTGT 60

RESULT 10
AC018903 214669 bp DNA linear HTG 04-JUN-2000
LOCUS Homo sapiens chromosome 15 clone RP11-337B11 map 15q21, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC018903
VERSION AC018903.2 GI:8247797
KEYWORDS HTG; HTGS_PHRASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 214669)
AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A.,
Madan,A., Nesbitt,R., Shafer,T. and Hood,L.
TITLE Sequencing of human chromosome 15 D15S146-D15S117 region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 214669)
AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shafer,T.
and Hood,L.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
COMMENT On Jun 4, 2000 this sequence version replaced gi:6630517.
----- Genome Center Sequence
Center: Multimegabase Sequencing Center
Center code: UMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leorowen@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; 108752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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* NOTE: This record contains 192 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 2069 2168: gap of unknown length
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* 6545 6645: gap of unknown length
* 6645 7472: contig of 828 bp in length
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* 44925 46114: contig of 1189 bp in length
* 46114 46214: gap of unknown length
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*	49277	50389:	contig	of 1113 bp in length
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*	50490	51333:	contig	of 844 bp in length
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*	58510	58609:	gap	of unknown length
*	58610	59745:	contig	of 1136 bp in length
*	59746	59845:	gap	of unknown length
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*	60556	60755:	gap	of unknown length
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*	62997	64138:	contig	of 1132 bp in length
*	64129	64228:	gap	of unknown length
*	64229	65025:	contig	of 798 bp in length
*	65027	65126:	gap	of unknown length
*	65127	66289:	contig	of 1143 bp in length
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*	68426	68525:	gap	of unknown length
*	68526	69322:	contig	of 797 bp in length
*	69323	69422:	gap	of unknown length
*	69423	70568:	contig	of 1146 bp in length
*	70569	70668:	gap	of unknown length
*	70669	71547:	contig	of 879 bp in length
*	71548	71647:	gap	of unknown length
*	71648	73629:	contig	of 1982 bp in length
*	73630	73729:	gap	of unknown length
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*	74588	74687:	gap	of unknown length
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*	77197	77296:	gap	of unknown length
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*	78552	78751:	gap	of unknown length
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*	79558	79657:	gap	of unknown length
*	79658	80774:	contig	of 1117 bp in length
*	80775	80874:	gap	of unknown length
*	80875	81690:	contig	of 816 bp in length
*	81691	81790:	gap	of unknown length
*	81791	82928:	contig	of 1138 bp in length
*	82929	83028:	gap	of unknown length
*	83029	83900:	contig	of 874 bp in length
*	83903	84002:	gap	of unknown length
*	84003	85193:	contig	of 1191 bp in length
*	85194	85293:	gap	of unknown length
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Query Match 5.3%; Score 47; DB 2; Length 214663;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
67 GGAGGCGCACCACTGGCGGACCCCGTGGGAGCGCACCGAGTGT 111

Db 74826 GGAGCGACACCATGGCCGACCGCTGCGGAGCGCACCGAGCTGT 74872

RESULT 11  
 BD18336/c  
 LOCUS BD18336 linear PAT 17-JUN-2003  
 DEFINITION Novel genes and proteins encoded by the genes.  
 ACCESSION BD18336  
 VERSION BD18336.1 GI:31875536  
 KEYWORDS JP 2002345492-A/49.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5147)  
 AUTHORS Ohara, O., Nagase, T. and Nakajima, D.  
 TITLE Novel genes and proteins encoded by the genes  
 JOURNAL Patent: JP 2002345492-A 49 03-DEC-2002;  
 KAZUSA DNA RESEARCH INSTITUTE  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002345492-A/49  
 PD 03-DEC-2002  
 PF 26-FEB-2002 JP 2002049009  
 PI OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA  
 PC C12N15/09, C07K14/47//A61K31/711, A61K38/00, A61P25/00, A61P25/14,  
 PC A61P25/18, A61P35/00, C12N15/00, A61K37/02  
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ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCTGGCTGCAGGCTCAGGCG 533  
 DB 4330 GCCTGGCTGCAGGCTCAGGCG 4309

RESULT 12  
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 LOCUS BD171150 linear PAT 17-JAN-2003  
 DEFINITION Novel gene and protein encoded thereby.  
 ACCESSION BD171150  
 VERSION BD171150.1 GI:27876962  
 KEYWORDS WO 02052005-A/6.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5147)  
 AUTHORS Ohara, O., Nagase, T. and Nakajima, D.  
 TITLE Novel gene and protein encoded thereby  
 JOURNAL Patent: WO 02052005-A 6 04-JUL-2002;  
 KAZUSA DNA RESEARCH INSTITUTE, OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA  
 COMMENT OS Homo sapiens (human)  
 PN WO 02052005-A/6  
 PD 04-JUL-2002  
 PF 20-DEC-2001 WO 2001JP011217  
 PR 22-DEC-2000 JP 00P 389742  
 PI OSAMU OHARA, TAKAHIRO NAGASE, DAISUKE NAKAJIMA  
 PC C12N15/12, C07K14/47  
 CC Novel gene and protein encoded thereby  
 CC Key Location/Qualifiers

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FEATURES
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ORIGIN
Query Match      2.5%; Score 22; DB 6; Length 5147;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCTGGCTGCAGGCTCAGGCG 533
Db 4330 GCCTGGCTGCAGGCTCAGGCG 4309

RESULT 13
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LOCUS      Homo sapiens mRNA for KIAA1654 protein, partial cds. PRI 06-OCT-2001
DEFINITION
ACCESSION  AB051441
VERSION     AB051441.1 GI:13359180
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hirosewa,M., Nagase,T., Murahashi,Y., Kikuno,R. and Ohara,O.
  TITLE     Identification of novel transcribed sequences on human chromosome
  JOURNAL   DNA Res. 8 (1), 1-9 (2001)
  MEDLINE   21156230
  PUBMED    11258795
REFERENCE   2 (bases 1 to 5147)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2000) Osamu Ohara, Kazusa DNA Research Institute,
  Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
  292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
  URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
  Fax:81-438-52-3914)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCTGGCTGCAGGCTCAGGCG 533
Db 4330 GCCTGGCTGCAGGCTCAGGCG 4309

RESULT 14

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LOCUS      Homo sapiens BCL2-interacting killer (apoptosis-inducing) (BIK)
DEFINITION
ACCESSION  AY245248
VERSION     AY245248.1 GI:28932927
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 21560)
  AUTHORS   Rieder,M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W.,
  Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
  Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-2003) Genome Sciences, University of Washington,
  1705 NE Pacific, Seattle, WA 98195, USA
  COMMENT   To cite this work please use: NIEHS-SNPs, Environmental Genome
  Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
  (URL: http://egp.gs.washington.edu).
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Qy 512 GCCTGGCTGAGGCTCAGGCG 533  
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 Db 9659 GCCTGGCTGAGGCTCAGGCG 9680

## RESULT 15

HS1191B2  
 LOCUS HS1191B2 60828 bp DNA linear PRI 05-JUN-2003  
 DEFINITION Human DNA sequence from clone CTB-1191B2 on chromosome  
 22q13.2-13.3, complete sequence.  
 ACCESSION AL022237  
 VERSION AL022237.1 GI:3845439  
 KEYWORDS HTG.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 60828)  
 AUTHORS Cobley, V.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Nov 5, 1998 this sequence version replaced gi:3820993.  
 COMMENT During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/projects/C-elegans/wormpep/CTB-1191B2 is  
 from the human BAC library described in U-J. Kim et al. (1996)  
 Genomics 34, 213-218.  
 VECTOR: pBelcBAC11  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquerry@sanger.ac.uk  
 -----  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e. phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest, except on the rare  
 occasion of the clone being a YAC.  
 This sequence was generated from part of bacterial clone contigs of  
 human chromosome 22, constructed by the Sanger Centre Chromosome 22  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr22  
 IMPORTANT: This sequence is not the entire insert of clone  
 CTB-1191B2. It may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true left end of clone CTB-1191B2 is at 1 in this sequence. The  
 true right end of clone RP3-323M22 is at 18859 in this sequence.

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repeat_region 10832. .10847
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repeat_region 10843. .11088
/note="113.0 copies 2 mer GT 141% conserved"
repeat_region 10853. .10899
/note="2.2 copies 21 mer GTGTGAGTACATGGGTGTCT 60%
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repeat_region 11135. .11150
/note="8.0 copies 2 mer TA 32% conserved"
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repeat_region 11523. .11886
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Query Match 2.5%; Score 22; DB 9; Length 60828;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCTGGCTCAGGCTCAGGCG 533
Db 33682 GCCTGGCTCAGGCTCAGGCG 33703
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Search completed: November 7, 2004, 04:47:20  
Job time : 6238 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 23:36:01 ; Search time 686 Seconds  
(without alignments)  
6787.517 Million cell updates/sec

Title: US-10-071-174-1  
Perfect score: 887  
Sequence: 1 cgggccaagaaacacgacga.....ctcttccttgactgaagaa 887

Scoring table: OLIGO\_NTC  
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_23sep04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001s:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	100.0	887	6	AAD46683 Human Bcl
2	763	86.0	1168	3	Aaz290049 Hydrophob
3	582	65.6	582	3	Aaz290039 Hydrophob
4	488	55.0	522	4	Aah47022 Human Bcl
5	225	25.4	548	4	Abk41913 cDNA enco
6	225	25.4	548	9	Abn59580 Connectiv
7	60	6.8	60	6	Abn42801 Human spl
8	24	2.7	24	6	Aad46685 Human Bcl
9	23	2.6	23	6	Aad46684 Human Bcl
10	22	2.5	22	6	Aad46689 Human Bcl
11	22	2.5	28	6	Aad46686 Human Bcl
12	22	2.5	34	6	Aad46688 Human Bcl
13	22	2.5	874	6	Abq44403 Oligonuel
14	22	2.5	874	6	Abq44402 Oligonuel
15	22	2.5	5147	6	Abn83959 Human gen
16	21	2.4	30	6	Aad46687 Human Bcl
17	21	2.4	3827	12	Adm66989 Murine ad
18	20	2.3	650	10	AdD34132 Mouse mit
19	20	2.3	823	4	Aak31741 Human cDN
20	20	2.3	823	4	Aak93761 Human cDN
21	20	2.3	823	12	AdL28168

22	20	2.3	823	12	ADL30188	AdL30188 3' end of
c	23	20	835	10	ADD34582	Add34582 Mouse mit
c	24	20	90798	12	ADP68859	Adp68859 Human chr
25	19	2.1	65	6	ABN30228	Abn30228 Rat splic
26	19	2.1	387	3	ADF56850	Adf56850 Urogenita
c	27	19	507	11	ABD15534	Abd15534 Pseudomon
28	19	2.1	665	6	ABT09478	Abt09478 Phase-1 R
29	19	2.1	665	10	ADG30917	Adg30917 Liver tox
30	19	2.1	665	12	ADG45503	Adg45503 Liver inf
c	31	19	936	11	ABD15622	Abd15622 Pseudomon
32	19	2.1	1630	2	AAQ28270	Aaq28270 Encodes r
33	19	2.1	1630	10	ABT41845	Abt41845 Toxicity
34	19	2.1	1779	5	AA578125	Aaa78125 DNA encod
35	19	2.1	3419	4	AA911196	Aaa911196 Mouse IGF
36	19	2.1	5561	6	AB192223	Abi92223 Mouse isc
c	37	19	9588	10	ADG37082	Adg37082 Vector pp
c	38	19	28198	10	ADG37080	Adg37080 Mouse pla
39	19	2.1	33053	6	ABQ67005	Abq67005 Human ang
40	19	2.1	143391	10	ADL13648	AdL13648 Osteoarth
c	41	18	421	8	ABX54335	Abx54335 Bovine ES
c	42	18	474	9	ACH18221	Ach18221 Human adu
43	18	2.0	530	3	AAF15017	Aaf15017 Trichoder
44	18	2.0	539	8	ABX91658	Abx91658 Murine ge
45	18	2.0	553	4	AAH13606	Aah13606 Human cDN

ALIGNMENTS

RESULT 1  
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ID AAD46683 standard; DNA; 887 BP.  
XX  
AC AAD46683;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Human Bcl-B DNA.  
XX  
KW Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder;  
KW proliferative disorder; muscle degeneration; Alzheimer's disease; CJD;  
KW Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic;  
KW Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia;  
KW SCA; dentatorubropallidoluysian atrophy; DRPLA; Kennedy's disease;  
KW stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnery;  
KW neurotropic; neuroprotective; cytostatic; immunosuppressive; vasotropic;  
KW cerebroprotective; autoimmune disorder; chromosome 15; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 50..664  
FT /tag= a  
FT /product= "Human Bcl-B protein"  
XX  
WO200272601-A2.  
XX  
PD 19-SEP-2002.  
XX  
XX 07-FEB-2002; 2002WO-US003547.  
XX  
XX 07-FEB-2001; 2001US-0267156P.  
XX 07-FEB-2002; 2002US-00071174.  
XX (BURN-) BURNHAM INST.  
XX Reed JC, Ke N, Godzik A;  
XX WPI; 2002-723312/78.  
XX P-PSDB; AAE23097.  
XX  
XX New isolated or recombinant Bcl-B nucleic acids and polypeptides, for  
XX treating a disorder associated with apoptosis, such as cell degenerative





Query Match		65.6%; Score 582; DB 3; Length 582;
Best Local Similarity		100.0%; Pred. No. 2.1e-277;
Matches 582; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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QY	140	GCCCGGAACCCGACCCCGAGCCGCCATCCAGCCCGAGCCCGCTGTGCGC 199
DB	61	GCCCGGAACCCGACCCCGAGCCGCCATCCAGCCCGAGCCCGCTGTGCGC 120
QY	200	TCCGCGCCCGCAGGTACCGAGATTCACCGGTCTCTTTCTCCGCTACCTCGGCTAC 259
DB	121	TCCGCGCCCGCAGGTACCGAGATTCACCGGTCTCTTTCTCCGCTACCTCGGCTAC 180
QY	260	CCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCTGTCTCCGACGCC 319
DB	181	CCCGGGAACCGCTTCGAGCTGGTGGCGCTGATGGCGGATTCCTGTCTCCGACGCC 240
QY	320	GGCCCCACCTGGGCGAGTGGTACGCTCTGTGACCTTCGACGAGCGCTGTGGAGAG 379
DB	241	GGCCCCACCTGGGCGAGTGGTACGCTCTGTGACCTTCGACGAGCGCTGTGGAGAG 300
QY	380	GGGCGCGTGTGACCGCCCGGTGAAGAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAG 439
DB	301	GGGCGCGTGTGACCGCCCGGTGAAGAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAG 360
QY	440	GAGGGCGAGTGGCCGGGACTGCGACGCGCTGGTGGCGCTTGTGAGCTCGCGCTCATG 499
DB	361	GAGGGCGAGTGGCCGGGACTGCGACGCGCTGGTGGCGCTTGTGAGCTCGCGCTCATG 420
QY	500	GGGCGAGCACCGCGCTGGCTGACGCTCAGGCGGCTGGATGGCTTTGTCACTTCTTC 559
DB	421	GGGCGAGCACCGCGCTGGCTGACGCTCAGGCGGCTGGATGGCTTTGTCACTTCTTC 480
QY	560	AGGACCCCTTTCCACTGGCTTTTGGAGAAACAGCTGTCCAGGCTTTTCTGTATGC 619
DB	481	AGGACCCCTTTCCACTGGCTTTTGGAGAAACAGCTGTCCAGGCTTTTCTGTATGC 540
QY	620	TTGTTAAACACAGCTTCATTATCTCTGGACAGGATTATTA 661
DB	541	TTGTTAAACACAGCTTCATTATCTCTGGACAGGATTATTA 582
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XX	AAH47022 standard; cDNA; 522 BP.	
AC	AAH47022;	
DT	29-OCT-2001 (first entry)	
DE	Human Bcl-2-like polypeptide encoding cDNA (clone HL1BE40).	
XX	Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;	
KW	respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;	
KW	immunosuppressive; antiinflammatory; gene therapy; ss.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
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FT		/note= "gene No. 2"
XX		
PN	W0200157060-A1.	
XX		
PD	09-AUG-2001.	
XX		
PF	31-JAN-2001; 2001WO-US003080.	
XX		

PR	01-FEB-2000; 2000US-0179487P.	
PR	07-FEB-2000; 2000US-0180697P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Ruben SM, Duan DR, Ni J;	
PI	WPI; 2001-476279/51.	
XX	P-PSDB; AAB85666.	
DR		
XX	Nucleic acids encoding human Bcl-2-like polypeptides, useful for	
PT	preventing, diagnosing and/or treating.	
PT	Claim 1; Page 276; 285pp; English.	
PS		
XX	The invention provides nucleic acid molecules (NAM1) encoding 4 human Bcl	
CC	-2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the	
CC	prevention, diagnosis and treatment of diseases associated with	
CC	inappropriate Bcl-2-like polypeptides' expression. The NAM1 may be used	
CC	to produce the soluble Bcl-2-like polypeptides by standard recombinant	
CC	methodology. The polypeptides may also be used as antigens in the	
CC	production of antibodies against Bcl-2 and in assays to identify	
CC	modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies	
CC	and antagonists may be used to down regulate expression and activity. The	
CC	anti-PEP1 antibodies may also be used as diagnostic agents for detecting	
CC	the presence of Bcl-2 polyps in samples (e.g. by enzyme linked	
CC	immunosorbant assay (ELISA)). Disorders that may be prevented, diagnosed	
CC	and/or treated by the above methods include, immunodeficiencies (e.g. a	
CC	gamma-globulinemia and B cell lymphoproliferative disorder), autoimmune	
CC	disorders (e.g. rheumatoid arthritis and Grave's disease), allergic	
CC	reactions, inflammations, respiratory diseases and cardiovascular	
CC	disorders (a full list of disorders is given in the specification). The	
CC	present sequence represents a human Bcl-2-like polypeptide encoding cDNA	
XX	Sequence 522 BP; 102 A; 148 C; 154 G; 118 T; 0 U; 0 Other;	
SQ		
	Query Match	55.0%; Score 488; DB 4; Length 522;
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	Matches 488; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	330	GGGGCAGAGTGGTGAAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAGAGGGCGGCTGG 389
DB	61	GGGGCAGAGTGGTGAAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAGAGGGCGGCTGG 120
QY	390	TGACCGCCCGGTGGAAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAGAGGGCGGCTGG 449
DB	121	TGACCGCCCGGTGGAAGTGGGGCTTCCAGCGCGGCTAAAGGAGCAGAGGGCGGCTGG 180
QY	450	TGCGCCGGGACTGCCAGCGCTGTGGCTTGTGAGCTCGCGCTCATGGGGCAGACCC 509
DB	181	TGCGCCGGGACTGCCAGCGCTGTGGCTTGTGAGCTCGCGCTCATGGGGCAGACCC 240
QY	510	GCGCTGCTGCTGAGGCTCAGGCGGCTGGGATGGCTTTTGTCACTTCTTCAGGACCCCT 569
DB	241	GCGCTGCTGCTGAGGCTCAGGCGGCTGGGATGGCTTTTGTCACTTCTTCAGGACCCCT 300
QY	570	TTCCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTTGTTAAACA 629
DB	301	TTCCACTGGCTTTTGGAGAAACAGCTGGTCCAGGCTTTTCTGTCATGCTTTGTTAAACA 360
QY	630	CAGCTTTCATTATCTCTGGACACGATTTATGAGTTTAAACTTTTAACTCCGCTTCT 689
DB	361	CAGCTTTCATTATCTCTGGACACGATTTATGAGTTTAAACTTTTAACTCCGCTTCT 420
QY	690	ACCTGCCCAACTGTGACCACTAAATGACAGATGTGTGAGAACAGAACTGAGGGAAGC 749
DB	421	ACCTGCCCAACTGTGACCACTAAATGACAGATGTGTGAGAACAGAACTGAGGGAAGC 480
QY	750	ACCTTCCC 757



```
Db      481 ACCTGCC 488
|||||
RESULT 5
ABK41913
ID   ABK41913 standard; cDNA; 548 BP.
XX
AC   ABK41913;
XX
DT   21-MAY-2002 (first entry)
XX
DE   cDNA encoding novel human connective tissue related polypeptide #301.
XX
KW   Human; connective tissue related disorder; cancer; gene therapy;
KW   cytoskeletal; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155343-A1.
XX
PD   02-AUG-2001.
XX
FF   17-JAN-2001; 2001WO-US001322.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
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PR   07-JUL-2000; 2000US-0216880P.
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PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   05-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   06-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241212P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   17-NOV-2000; 2000US-0249213P.
PR   17-NOV-2000; 2000US-0249214P.
PR   17-NOV-2000; 2000US-0249215P.
PR   17-NOV-2000; 2000US-0249216P.
PR   17-NOV-2000; 2000US-0249217P.
PR   17-NOV-2000; 2000US-0249218P.
PR   17-NOV-2000; 2000US-0249244P.
PR   17-NOV-2000; 2000US-0249245P.
PR   17-NOV-2000; 2000US-0249246P.
PR   17-NOV-2000; 2000US-0249265P.
PR   17-NOV-2000; 2000US-0249297P.
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PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251388P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 05-DEC-2000; 2000US-0251479P.  
 PR 05-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX WPI; 2001-565190/63.  
 DR P-PSDB; AAU86735.  
 DR  
 XX Nucleic acid encoding novel connective tissue associated polypeptides,  
 PT used in diagnosing, preventing, treating or ameliorating a disorder such  
 PT as cancer or rheumatoid arthritis.  
 PT  
 XX Claim 4; SEQ ID NO 311; 673pp; English.  
 PS  
 XX The present invention relates to the isolation of novel human connective  
 CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide  
 CC (cDNA and genomic) sequences encoding them. The sequences of the  
 CC invention are useful in the diagnosis, treatment, prevention and/or  
 CC prognosis of diseases associated with connective tissue(s), including  
 CC cancer. The polynucleotide sequences of the invention are also useful in  
 CC gene therapy. ABK41613-ABK42101 represent cDNA sequences encoding the  
 CC novel human connective tissue related polypeptides. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 548 BP; 99 A; 154 C; 167 G; 121 T; 0 U; 7 Other;  
 SQ  
 Query Match 25.4%; Score 225; DB 4; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-101;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 524 GCTCAGGCGCGTGGATGGCTTTTGTCACTTCTTCAGGACCCCTTCCACTGGCTTTT 583  
 Db 324 GCTCAGGCGCGTGGATGGCTTTTGTCACTTCTTCAGGACCCCTTCCACTGGCTTTT 383  
 Qy 584 TGGAGAAAACAGCTGGTCCAGGCTTTTCTCTCATGCTTGTAAACACAGCTTCAATTAT 643  
 Db 384 TGGAGAAAACAGCTGGTCCAGGCTTTTCTCTCATGCTTGTAAACACAGCTTCAATTAT 443  
 Qy 644 CTCTGGACAGCATTAATATGAGTTTAAACTTTTAAACCGCTTCTACCTGCCCACTGT 703  
 Db 444 CTCTGGACAGCATTAATATGAGTTTAAACTTTTAAACCGCTTCTACCTGCCCACTGT 503  
 Qy 704 GACCACTAAATGACAGATGTGAGAACAGAACTGAGGGAAG 748  
 Db 504 GACCACTAAATGACAGATGTGAGAACAGAACTGAGGGAAG 548  
 RESULT 6  
 ID ADB59580 standard; cDNA; 548 BP.  
 XX  
 XX ADB59580;  
 XX  
 XX 04-DEC-2003 (first entry)  
 XX  
 DE Connective tissue related polynucleotide #301.

XX cyrostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;  
 KW antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritis;  
 KW antiinflammatory; antiallergic; antiasthmatic; dermatological;  
 KW nephrotropic; virucide; fungicide; antibacterial; antiparasitic;  
 KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;  
 KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;  
 KW cancer metastasis; neoplasia; leukemia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;  
 KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;  
 KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;  
 KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;  
 KW gastrointestinal disorder; inflammatory bowel disease;  
 KW organ transplant rejection; immune system disorder; Bruton's disease;  
 KW X-linked lymphoproliferative syndrome;  
 KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;  
 KW chromosome identification; chromosome mapping;  
 KW connective tissue related polynucleotide; gene; ss.  
 XX Homo sapiens.  
 XX  
 XX US2003054375-A1.  
 PN  
 XX 20-MAR-2003.  
 PD  
 XX 07-MAR-2002; 2002US-00092154.  
 PF  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 27-JUN-2000; 2000US-0209457P.  
 PR 28-JUN-2000; 2000US-0214866P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218230P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225287P.  
 PR 14-AUG-2000; 2000US-0225288P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225575P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 09-SEP-2000; 2000US-0231243P.



```

AC ABN42801;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:15549.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-1B001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX PR 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of a
XX PT genome useful for detecting tissue-, pathology-, and developmental-
XX PT specific genes.
XX
XX Example 1; SEQ ID NO 15549; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX CC )transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises several
XX CC oligonucleotides, each capable of hybridizing selectively to a set of
XX CC messenger RNAs transcribed from a given transcription unit of the genome,
XX CC which encodes one or more messenger RNA splice variants. The
XX CC oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterizing the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialized mini
XX CC libraries to detect transcripts of a sub-transcriptome under a particular
XX CC biological or pathological state, and so allowing the detection of tissue
XX CC - and pathology-specific genes such as those genes only expressed in
XX CC specific tissue under a specific pathological condition; to detect
XX CC developmental specific genes; and to detect RNA transcripts and splice
XX CC variants of a transcriptome of a patient suffering from a particular
XX CC disorder. ABN27253 to ABN59588 represent oligonucleotide sequences from
XX CC rats, humans and mice, which are used in the exemplification of the
XX CC present invention. N.B. The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60 BP; 9 A; 16 C; 13 G; 22 T; 0 U; 0 Other;
XX
XX Query Match 6.8%; Score 60; DB 6; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 4.4e-19;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 565 CCCCTTCCACTGCTTTTGGAGAAACACAGCTGGTCCAGGCTTTTCTGTCATGCTTGT 624
XX 1 CCCCTTCCACTGCTTTTGGAGAAACACAGCTGGTCCAGGCTTTTCTGTCATGCTTGT 60
XX
XX RESULT 8
XX AAD46685/C
XX ID AAD46685 standard; DNA; 24 BP.
XX
XX AAD46685;
XX

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XX
XX 27-JAN-2003 (first entry)
XX
XX Human Bcl-B cDNA cloning reverse RT-PCR primer, NK0121.
XX
XX Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder;
XX KW proliferative disorder; muscle degeneration; Alzheimer's disease; CJD;
XX KW Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic;
XX KW Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia;
XX KW SCA; dentatorubralpallidoluysian atrophy; DRPLA; Kennedy's disease;
XX KW stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnery;
XX KW neurotropic; neuroprotective; cytostatic; immunosuppressive; vasotropic;
XX KW cerebroprotective; autoimmune disorder; reverse transcription; RT; PCR;
XX KW primer; ss.
XX
XX Homo sapiens.
XX
XX WO200272601-A2.
XX
XX 19-SEP-2002.
XX
XX 07-FEB-2002; 2002WO-US003547.
XX
XX 07-FEB-2001; 2001US-0267166P.
XX PR 07-FEB-2002; 2002US-00071174.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Ke N, Godzik A;
XX
XX WPI; 2002-723312/78.
XX
XX New isolated or recombinant Bcl-B nucleic acids and polypeptides, for
XX PT treating a disorder associated with apoptosis, such as cell degenerative
XX PT or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's
XX PT disease.
XX
XX Example 1; Page 47; 82pp; English.
XX
XX The invention relates to human member of Bcl-2 family Bcl-B protein and
XX CC its corresponding nucleic acid. Bcl-B is useful in treating a subject
XX CC having or at risk of a disorder associated with apoptosis, such as cell
XX CC degenerative or proliferative disorder like neural or muscle
XX CC degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease
XX CC (CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's
XX CC disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6),
XX CC dentatorubralpallidoluysian atrophy (DRPLA), Kennedy's disease, stroke,
XX CC ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic
XX CC condition. The transgenic animals are used as in vivo models to study
XX CC apoptosis and potential therapies for apoptosis. The present sequence is
XX CC a reverse transcription (RT)-PCR primer used for cloning human Bcl-B cDNA
XX
XX Sequence 24 BP; 8 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 24; DB 6; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 0.3;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 858 ATGCAATGGCTCTTCCTTGAGTG 881
XX 24 ATGCAATGGCTCTTCCTTGAGTG 1
XX
XX RESULT 9
XX AAD46684
XX ID AAD46684 standard; DNA; 23 BP.
XX
XX AAD46684;
XX
XX 27-JAN-2003 (first entry)
XX
XX Human Bcl-B cDNA cloning forward RT-PCR primer, NK01.
XX

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Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder; Proliferative disorder; muscle degeneration; Alzheimer's disease; CUD; Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic; Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia; SCA; dentatorubralpallidoluysian atrophy; DRPLA; Kennedy's disease; stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnary; neurotropic; neuroprotective; cytostatic; immunosuppressive; vasotropic; cerebroprotective; autoimmune disorder; reverse transcription; RT; PCR; primer; ss.	Human sapiens.	OS	XX
WO200272601-A2.	WO200272601-A2.	PN	XX
19-SEP-2002.	19-SEP-2002.	PD	XX
07-FEB-2002; 2002WO-US003547.	07-FEB-2002; 2002WO-US003547.	PF	XX
07-FEB-2001; 2001US-0267166P.	07-FEB-2001; 2001US-0267166P.	PR	XX
07-FEB-2002; 2002US-00071174.	07-FEB-2002; 2002US-00071174.	PR	XX
(BURN-) BURNHAM INST.	(BURN-) BURNHAM INST.	PA	XX
Reed JC, Ke N, Godzik A;	Reed JC, Ke N, Godzik A;	PI	XX
WPI; 2002-723312/78.	WPI; 2002-723312/78.	DR	XX
New isolated or recombinant Bcl-B nucleic acids and polypeptides, for treating a disorder associated with apoptosis, such as cell degenerative or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's disease.	New isolated or recombinant Bcl-B nucleic acids and polypeptides, for treating a disorder associated with apoptosis, such as cell degenerative or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's disease.	PT	XX
Example 1; Page 47; 82pp; English.	Example 1; Page 47; 82pp; English.	PP	XX
The invention relates to human member of Bcl-2 family Bcl-B protein and its corresponding nucleic acid. Bcl-B is useful in creating a subject having or at risk of a disorder associated with apoptosis, such as cell degenerative or proliferative disorder like neural or muscle degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease (CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6), dentatorubralpallidoluysian atrophy (DRPLA), Kennedy's disease, stroke, ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic condition. The transgenic animals are used as in vivo models to study apoptosis and potential therapies for apoptosis. The present sequence is a reverse transcription (RT)-PCR primer used for cloning human Bcl-B cDNA	The invention relates to human member of Bcl-2 family Bcl-B protein and its corresponding nucleic acid. Bcl-B is useful in creating a subject having or at risk of a disorder associated with apoptosis, such as cell degenerative or proliferative disorder like neural or muscle degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease (CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6), dentatorubralpallidoluysian atrophy (DRPLA), Kennedy's disease, stroke, ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic condition. The transgenic animals are used as in vivo models to study apoptosis and potential therapies for apoptosis. The present sequence is a reverse transcription (RT)-PCR primer used for cloning human Bcl-B cDNA	Sequence 23 BP; 9 A; 6 C; 8 G; 0 T; 0 U; 0 Other;	XX
Query Match	2.6%; Score 23; DB 6; Length 23;		
Best Local Similarity	100.0%; Pred. No. 0.94;		
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CGGGCCACAGAAACCCAGCGAAGG 23		
Db	1 CGGGCCACAGAAACCCAGCGAAGG 23		
RESULT 10			
AAD46689			
ID	AAD46689 standard; DNA; 22 BP.		
AC	AAD46689;		
AC			
XX			
DT	27-JAN-2003 (first entry)		
DE	Human Bcl-B cDNA amplifying forward RT-PCR primer, NK0120.		
XX			
Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder; Proliferative disorder; muscle degeneration; Alzheimer's disease; CUD; Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic; Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia; SCA; dentatorubralpallidoluysian atrophy; DRPLA; Kennedy's disease;	Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder; Proliferative disorder; muscle degeneration; Alzheimer's disease; CUD; Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic; Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia; SCA; dentatorubralpallidoluysian atrophy; DRPLA; Kennedy's disease;		

KW	stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnary;
KW	neotrophic; neuroprotective; cytostatic; immunosuppressive; vasotropic;
KW	cerebroprotective; autoimmune disorder; reverse transcription; RT; PCR;
KW	primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200272601-A2.
XX	
XX	
PD	19-SEP-2002.
XX	
XX	
PF	07-FEB-2002; 2002WO-US003547.
XX	
XX	
PR	07-FEB-2001; 2001US-0267166P.
PR	07-FEB-2002; 2002US-00071174.
XX	
XX	(BURN-) BURNHAM INST.
XX	
PI	Reed JC, Ke N, Godzik A;
XX	
DR	WPI; 2002-723312/78.
XX	
XX	
PT	New isolated or recombinant Bcl-B nucleic acids and polypeptides, for
PT	treating a disorder associated with apoptosis, such as cell degenerative
PT	or proliferative disorder e.g. cancer, Alzheimer's disease or Parkinson's
PT	disease.
XX	
PS	Example 1; Page 48; 82pp; English.
XX	
CC	The invention relates to human member of Bcl-2 family Bcl-B protein and
CC	its corresponding nucleic acid. Bcl-B is useful in treating a subject
CC	having or at risk of a disorder associated with apoptosis, such as cell
CC	degenerative or proliferative disorder like neural or muscle
CC	degeneration, e.g. Alzheimer's disease, Creutzfeldt-Jacob's disease
CC	(CJD), Machado-Joseph disease (MJD), Parkinson's disease, Huntington's
CC	disease (HD), spinocerebellar ataxias 1, 2 and 6 (SCA-1, -2 and -6),
CC	dentatorubropallidolysian atrophy (DRPLA), Kennedy's disease, stroke,
CC	ischaemia, head trauma, neoplasia, autoimmune disorder or fibrotic
CC	condition. The transgenic animals are used as in vivo models to study
CC	apoptosis and potential therapies for apoptosis. The present sequence is
CC	a reverse transcription (RT)-PCR primer used for amplifying human Bcl-B
CC	cDNA
XX	
XX	
SQ	Sequence 22 BP; 2 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
	Query Match 2.5%; Score 22; DB 6; Length 22;
	Best Local Similarity 100.0%; Pred. No. 2.9;
	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	338 GTGGTGACGCTCGTGACCTTCG 359
Db	1 GTGGTGACGCTCGTGACCTTCG 22
RESULT 11	
AD46686	
ID	AAD46686 standard; DNA; 28 BP.
XX	
AC	AAD46686;
XX	
DT	27-JAN-2003 (first entry)
XX	
DE	Human Bcl-B DNA amplifying forward PCR primer, NK0101.
XX	
KW	Human; Bcl-2; Bcl-B; therapy; apoptosis; cell degenerative disorder;
KW	proliferative disorder; muscle degeneration; Alzheimer's disease; CJD;
KW	Creutzfeldt-Jacob's disease; Machado-Joseph disease; MJD; transgenic;
KW	Parkinson's disease; Huntington's disease; HD; spinocerebellar ataxia;
KW	SCA; dentatorubropallidolysian atrophy; DRPLA; Kennedy's disease;
KW	stroke; ischaemia; head trauma; neoplasia; anticonvulsant; vulnary;
KW	neotrophic; neuroprotective; cytostatic; immunosuppressive; vasotropic;
KW	cerebroprotective; autoimmune disorder; PCR; primer; ss.
XX	



XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX Sequence 874 BP; 374 A; 291 C; 90 G; 119 T; 0 U; 0 Other;  
SQ Query Match 2.5%; Score 22; DB 6; Length 874;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 233 TCCTTTTCTCCGCTACCTCG 254  
DB 332 TCCTTTTCTCCGCTACCTCG 353  
RESULT 14  
ABQ4402/c  
ID ABQ4402 standard; DNA; 874 BP.  
AC ABQ4402;  
XX 12-JUL-2002 (first entry)  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 30993.  
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX Homo sapiens.  
XX WO200218632-A2.  
XX 07-MAR-2002.  
XX 01-SEP-2001; 2001WO-EP010074.  
XX 01-SEP-2000; 2000DE-01043826.  
XX 05-SEP-2000; 2000DE-01044543.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons

PT from chemically treated DNA.  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX Sequence 874 BP; 119 A; 90 C; 291 G; 374 T; 0 U; 0 Other;  
SQ Query Match 2.5%; Score 22; DB 6; Length 874;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 233 TCCTTTTCTCCGCTACCTCG 254  
DB 543 TCCTTTTCTCCGCTACCTCG 522  
RESULT 15  
ABN83959/c  
ID ABN83959 standard; DNA; 5147 BP.  
XX AC ABN83959;  
XX 06-SEP-2002 (first entry)  
XX Human gene sequence #6.  
XX Human; brain; tonsil; hippocampus; foetal brain; diagnosis; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 2074..2349  
FT /\*tag=a  
FT /partial  
FT /note= "no start codon present"  
XX WO200252005-A1.  
XX 04-JUL-2002.  
XX 20-DEC-2001; 2001WO-JP011217.  
XX 22-DEC-2000; 2000JP-00389742.  
XX (KAZU-) KAZUSA DNA RES INST FOUND.  
XX (CELE-) CELESTAR LEXICO-SCI LTD.  
XX Ohara O, Nagase T, Nakajima D;  
XX WPI; 2002-500762/53.  
XX P-PSDB; ABB97939.  
XX Genes and their expression products cloned from human cDNA libraries for

```

PT treatment and diagnosis of diseases associated with their expression.
XX Claim 1(a); Page 63-66; 238pp; Japanese.
XX The invention relates to DNA encoding polypeptides directly cloned from
CC cDNA libraries originating in adult whole brain, human tonsil, human
CC adult hippocampus and human foetal whole brain. Polypeptides and
CC polynucleotides of the invention may be used in the investigation of
CC differential expression of the DNA sequences in normal subjects and
CC disease patients. They may also be used in the production of antibodies,
CC oligonucleotide probes and DNA chips for diagnosis and identification of
CC drugs for treatment of diseases with which the DNA sequences are
CC associated. The sequences given in records ABN83954-ABN83984 represent
CC human gene sequences of the invention
XX
XX Sequence 5147 BP; 1212 A; 1455 C; 1334 G; 1146 T; 0 U; 0 Other;
SQ Query Match 2.5%; Score 22; DB 6; Length 5147;
Best Local Similarity 100.0%; Pred.No.2.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 512 GCCTGGGCTGCAGGCTCAGGGCG 533
| | | | |
| | | | |
Db 4330 GCCTGGGCTGCAGGCTCAGGGCG 4309

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 02:37:47 ; Search time 4548 Seconds  
(without alignments)  
7106.869 Million cell updates/sec

Title: US-10-071-174-1

Perfect score: 887

Sequence: 1 cgggccaagaaaccagcga.....ctcttccttgagtgaagaa 887

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gssi:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	197	22.2	715	6	CA777633 ip19a09.y
C 2	167	18.8	535	5	EX119239
C 3	111	12.5	493	1	A1813346
C 4	91	10.3	130	1	AA098865
C 5	53	6.0	206	1	AA005293
C 6	30	3.4	478	7	R53538
C 7	27	3.0	939	9	CNS32COP
C 8	22	2.5	316	7	R85550
C 9	22	2.4	441	8	BZ865242
C 10	21	2.4	441	8	AZ617122
C 11	21	2.4	462	5	BY590905
C 12	21	2.4	479	8	AQ294438
C 13	21	2.4	494	1	AA823641
C 14	21	2.4	657	2	BB628603
C 15	21	2.4	803	9	CNS04135
C 16	21	2.4	881	2	BF532088
C 17	21	2.4	931	4	BG173025
C 18	21	2.4	2780	3	AK035932
C 19	20	2.3	352	1	AA426934
C 20	20	2.3	415	5	BY059827
C 21	20	2.3	448	6	CA560084
C 22	20	2.3	454	1	AJ631643
C 23	20	2.3	455	8	AQ457939
C 24	20	2.3	478	6	CA561864

#### ALIGNMENTS

RESULT 1  
CA777633/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CA777633 715 bp mRNA linear EST 03-DEC-2002  
ip19a09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6217625 5'  
similar to TR:Q9Z0F3 Q9Z0F3 BCL-2 HOMOLOG. ; mRNA sequence.

CA777633  
CA777633.1 GI:26015508  
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 715)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J.,  
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R.,  
Williams,T., Jackson,Y., and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@wustl.edu)

Possible reversed clone: similarity on wrong strand

Seq primer: -403p from Gibco

High quality sequence stop: 392.

#### FEATURES

source

Location/Qualifiers

1..715  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:6217625"  
/tissue\_type="Purified pancreatic islet"  
/lab\_host="DH10B"  
/clone\_lib="HR85 islet"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1;  
NotI; Site 2: XhoI; cDNA made by oligo-dr priming.

Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

## ORIGIN

Query Match 22.2%; Score 197; DB 6; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-95;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 CTTGCCCACTGTGACCACTAAATGACAGATGTGTGAGAACAACTGAGGAAAGCA 750  
 Db 581 CTTGCCCACTGTGACCACTAAATGACAGATGTGTGAGAACAACTGAGGAAAGCA 522  
 QY 751 CTTTCCCCCACCAGACGTTTTATCTGAATGCATACAGGAGTCTCTGAGGTGGTATT 810  
 Db 521 CTTTCCCCCACCAGACGTTTTATCTGAATGCATACAGGAGTCTCTGAGGTGGTATT 462  
 QY 811 TGGCCAGTGTTTAACTGTGACAAGTACTCAGGTGTGAGGACAAGATGCAAAATGGCTC 870  
 Db 461 TGGCCAGTGTTTAACTGTGACAAGTACTCAGGTGTGAGGACAAGATGCAAAATGGCTC 402  
 QY 871 TTCCTTGAGTGAAGAA 887  
 Db 401 TTCCTTGAGTGAAGAA 385

## RESULT 2

BX119239/c  
 LOCUS BX119239 535 bp mRNA linear EST 10-FEB-2003  
 DEFINITION BX119239 Soares infant brain IN1B Homo sapiens cDNA clone  
 IMAGP998N01170 ; IMAGE:40052, mRNA sequence.  
 ACCESSION BX119239  
 VERSION BX119239.1 GI:27841652  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 535)  
 AUTHORS Ebert L., Heil O., Hennig S., Neubert P., Partsch E., Peters M.,  
 Radlof U., Schneider D. and Korn B.

TITLE Human Unigeneset - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP998N01170.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/Clonecards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (Clone@rzpd.de) for further information. Seq primer:  
 M13u, Primer sequence: CCGTGAACACGACGCCAGT.

## FEATURES

source  
 1..535  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /c.clone="IMAGP998N01170 ; IMAGE:40052"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_hosts="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares infant brain IN1B"

## ORIGIN

Query Match 19.8%; Score 167; DB 5; Length 535;  
 Best Local Similarity 100.0%; Pred. No. 1e-78;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ATGTGTGAGAACAAAGAACTGAGGAAAGACCTTCCCCACCCAGACGTTTTTATCTGA 780  
 Db 535 ATGTGTGAGAACAAAGAACTGAGGAAAGACCTTCCCCACCCAGACGTTTTTATCTGA 476  
 QY 781 ATGCATACAGGAGTCTCTGAGGTGGTATTGGCCAGTGTTTAACTGTGACAAGTACT 840  
 Db 475 ATGCATACAGGAGTCTCTGAGGTGGTATTGGCCAGTGTTTAACTGTGACAAGTACT 416  
 QY 841 CAGGTGTGAGGACAAAGAAATGCAATGGCTCTCTCCCTGAGTGAAGAA 887  
 Db 415 CAGGTGTGAGGACAAAGAAATGCAATGGCTCTCTCCCTGAGTGAAGAA 369

## RESULT 3

AI813346/c  
 LOCUS AI813346 493 bp mRNA linear EST 21-DEC-1999  
 DEFINITION wj33903.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2404660 3',  
 mRNA sequence.  
 ACCESSION AI813346  
 VERSION AI813346.1 GI:5424561  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 493)  
 AUTHORS NCI-CGAP  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@pse-mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 879 Scd Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 447.  
 Location/Qualifiers  
 1..493  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /c.clone="IMAGE:2404660"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_hosts="DH10B"  
 /clone\_lib="NCI\_CGAP\_Kid12"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs

## FEATURES

source  
 1..493  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /c.clone="IMAGE:2404660"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_hosts="DH10B"  
 /clone\_lib="NCI\_CGAP\_Kid12"  
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs

/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not  
 1; Site 2: Hind III; 1st strand cDNA was primed with a Not  
 I - oligo(dT) primer [5',  
 AACTGGAAGAAATTCGGCGCCGACGAGATTTTTTTTTTTT 3'];  
 Double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Lafmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaudo."

from a pool of 5,000 clones made from the same library  
(clonides 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo. "

## ORIGIN

Query Match 12.5%; Score 111; DB 1; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.6e-48;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 777 CTGAATGCATACAGAGTCCTGAGGTGGTGTGATTTGGCCAGTGTGTTAACTTGTGACAAAG 836  
|||||  
DB 469 CTGAATGCATACAGAGTCCTGAGGTGGTGTGATTTGGCCAGTGTGTTAACTTGTGACAAAG 410  
|||||  
QY 837 TACTCAGGTGTGAGGCAAGATGCAATGGCTCTCTCTTGGAGTGAAGAA 887  
|||||  
DB 409 TACTCAGGTGTGAGGCAAGATGCAATGGCTCTCTCTTGGAGTGAAGAA 359  
|||||

RESULT 4  
AA098865 130 bp mRNA linear EST 28-OCT-1996  
LOCUS zK84f02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone  
DEFINITION IMAGE:489531 3', mRNA sequence.

ACCESSION AA098865  
VERSION  
KEYWORDS  
SOURCE

ORGANISM Homo sapiens (human)

EST.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 130)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 81.

## FEATURES

source

1..130  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3804118"  
/db\_xref="taxon:9606"  
/clone="IMAGE:489531"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"  
/note="Organ: uterus; Vector: pT73-Pac; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5',  
AAGTGAAGATTCGCGCGCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by M. Fatima Bonaldo."

## ORIGIN

Query Match 10.3%; Score 91; DB 1; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.7e-37;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 242 TCGCCTTACCTCGCTACCCCGGAAACCGCTTCGAGTGTGCGGTGATGGCGGATTC 301  
|||||  
DB 1 TCGCCTTACCTCGCTACCCCGGAAACCGCTTCGAGTGTGCGGTGATGGCGGATTC 60  
|||||  
QY 302 GTGCTCTCCACAGCCCCCGCCACCTGGG 332  
|||||  
DB 61 GTGCTCTCCACAGCCCCCGCCACCTGGG 91  
|||||

RESULT 5  
AA005293 206 bp mRNA linear EST 07-MAY-1997  
LOCUS zh93a11.r1 Soares fetal\_liver\_spleen\_INFLS\_S1 Homo sapiens cDNA  
DEFINITION clone IMAGE:428828 5', mRNA sequence.

ACCESSION AA005293

VERSION

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 206)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.

and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

8889549

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 849 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 126.

## FEATURES

source

1..206  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1328597"  
/db\_xref="taxon:9606"  
/clone="IMAGE:428828"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal\_liver\_spleen\_INFLS\_S1"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
This is a subtracted version of the original Soares fetal  
liver spleen INFUS library. 1st strand cDNA was primed  
with a Pac I - oligo(dT) primer [5',  
AAGTGAAGATTCGCGCGCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 6.0%; Score 53; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Insert Size: 1578  
High quality sequence stops: 278  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1578 Std Error: 0.00  
Seq primer: Promega -21ml3  
High quality sequence stop: 278.

#### FEATURES

1..316  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GBB:3826849"  
/db\_xref="taxon:9606"  
/clone="IMAGE:180205"  
/sex="Male"  
/dev\_stage="55-year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares adult brain N2b4HB55y"  
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaudo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

#### ORIGIN

Query Match 2.5%; Score 22; DB 7; Length 316;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 GCCTGGCTGCAGGCTCAGGCGC 533  
|||||  
Db 212 GCCTGGCTGCAGGCTCAGGCGC 233  
|||||

RESULT 9  
BZ869242 601 bp DNA linear GSS 18-MAR-2003  
LOCUS  
DEFINITION  
CH240\_211K10.TJ CHORI-240 Bos taurus genomic clone CH240\_211K10,  
genomic survey sequence.  
ACCESSION  
BZ869242  
VERSION  
BZ869242.1 GI:29096647  
KEYWORDS  
GSS.  
SOURCE  
Bos taurus (cow)  
ORGANISM  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

#### REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 601)  
Zhao, S., Shetty, J., Shatsman, S., Teegay, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A. M. and McEwan, J. C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.  
Plate: 211 row: K column: 10  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

Location/Qualifiers  
1..601  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_211K10"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pFARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull LI Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

#### ORIGIN

Query Match 2.5%; Score 22; DB 8; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.3;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 GAAAGCACCTTCCCCACCCCA 765  
|||||  
Db 229 GAAAGCACCTTCCCCACCCCA 250  
|||||

#### RESULT 10 AZ617122/c LOCUS

DEFINITION  
1M0448D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0448D17 F, genomic survey sequence.  
ACCESSION  
AZ617122  
VERSION  
AZ617122.1 GI:11739312  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE AUTHORS

1 (bases 1 to 441)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, I., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dcunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0448 row: D column: 17  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 441.

## FEATURES

Location/Qualifiers  
 1..441  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0448D1.7"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWB42 (G14732114|GP|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 2.4%; Score 21; DB 8; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 GAGAAACACCTGGTCAGGC 606

Db 276 GAGAAACACCTGGTCAGGC 256

## RESULT 11

BY590905/c 462 bp mRNA linear EST 15-DEC-2002  
 LOCUS BY590905 RIKEN full-length enriched, adult inner ear Mus musculus  
 DEFINITION cDNA clone F930014102 3', mRNA sequence.  
 ACCESSION BY590905  
 VERSION BY590905.1 GI:26926087  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 462)

## REFERENCE

AUTHORS  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schönbach, C., Cojocari, T., Baldarelli, R., Hill, D. P., Buit, C.,  
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,  
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,  
 Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedierski, R. M., King, B. L., Konagaya, A.,  
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

## TITLE

JOURNAL  
 MEDLINE  
 PUBMED

## COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN,  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Kirk W. Beisel ( Boys Town National  
 Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.

## FEATURES

Location/Qualifiers  
 1..462  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="F930014102"  
 /tissue\_type="inner ear"  
 /dev\_stage="adult"  
 /clone\_lib="RIKEN full-length enriched, adult inner ear"

## ORIGIN

Query Match 2.4%; Score 21; DB 5; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 748 GCACCTTCCCCCAGCCAGAC 768

Thising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:615218  
High quality sequence stop: 493.  
Location/Qualifiers  
1. .494  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CE7BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1125882"  
/tissue\_type="embryo"  
/dev\_stage="2-cell"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse 2 cell"  
/note="Organ: embryo; Vector: pBluescribe (modified);  
Site:1: MluI; Site:2: SalI; Cloned unidirectionally from  
mRNA prepared from 13,500 2-cell stage embryos. Primer:  
SalI (drt): 5'-CGGTCCAGCTGCACCGTTTTTTTTTTT-3'. CDNAS  
were cloned into the MluI/SalI sites of a modified  
pBluescribe vector using commercial linkers (NEB).  
Average insert size: 1.2 kb."

2.4%; Score 21; DB 1; Length 494;  
Similarity 100.0%; Pred. No. 18;  
21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

48 GCACCTTCCCCCACCACCGAC 768  
|||||  
55 GCACCTTCCCCCACCACCGAC 385  
|||||

657 bp mRNA linear EST 26-OCT-2000  
RIKEN full-length enriched, 16 days neonate cerebellum Mmu  
musculus cDNA clone 9630018N03 5', mRNA sequence.  
BB528603.1 GI:16465993  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria;  
1 (bases 1 to 657)  
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,  
Hata,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,  
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,  
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,  
Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
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Tel: 81-45-503-9222  
Fax: 81-45-503-9216

